

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2006, 06:54:58 ; Search time 5124 Seconds
(without alignments)
10317.020 Million cell updates/sec

Title: US-09-825-882-7

Perfect score: 930

Sequence: 1 atgataacttttctaccat.....agaagacttcctccatag 930

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 583141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 930 | 100.0 | 930 | 8 | AY114089 Homo sapi |
| 3 | 930 | 100.0 | 1330 | 6 | AX647299 Sequence |
| 4 | 930 | 100.0 | 110000 | 14 | AC018743 0 |
| 5 | 930 | 100.0 | 167868 | 8 | AC018630 Homo sapi |
| 6 | 925.2 | 99.5 | 930 | 8 | AY724943 Homo sapi |
| 7 | 924 | 99.4 | 930 | 6 | CS008113 Sequence |
| 8 | 923.2 | 99.3 | 930 | 8 | AF494237 Homo sapi |
| 9 | 922.2 | 99.2 | 927 | 6 | CQ800006 Sequence |
| 10 | 917.2 | 98.6 | 930 | 8 | AY724889 Pan trogl |
| 11 | 915.2 | 98.4 | 930 | 8 | AY677147 Pan panis |
| 12 | 865.6 | 93.1 | 930 | 8 | AY724849 Pan panis |
| 13 | 863.6 | 92.9 | 870 | 8 | AY736059 Pan trogl |
| 14 | 861.2 | 92.6 | 930 | 8 | AY724878 Pan trogl |
| 15 | 859.2 | 92.4 | 930 | 8 | AY677148 Pan panis |
| 16 | 858 | 92.3 | 930 | 8 | AY724974 Pongo pyg |
| 17 | 857 | 92.2 | 857 | 8 | AB199182 Homo sapi |
| 18 | 853.2 | 91.7 | 930 | 8 | AY724942 Homo sapi |

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| 23 | 851.2 | 91.5 | 930 | 6 | CS008275 Sequence |
| 24 | 851.2 | 91.5 | 930 | 8 | AF494228 Homo sapi |
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| 26 | 850.2 | 91.4 | 927 | 6 | CQ800008 Sequence |
| 27 | 849.6 | 91.4 | 930 | 6 | CS008271 Sequence |
| 28 | 849.6 | 91.4 | 930 | 6 | CS008277 Sequence |
| 29 | 848 | 91.2 | 930 | 6 | CS008273 Sequence |
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| 45 | 825.6 | 88.8 | 888 | 8 | AY736056 Pan trogl |

ALIGNMENTS

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LOCUS BD144616
DEFINITION Novel G-protein coupled receptors.
ACCESSION BD144616
VERSION BD144616.1 GI:27850374
KEYWORDS JP 2002112793-A/341.
SOURCE Homo sapiens (human)
ORIGIN Homo sapiens

linear PAT 17-JAN-2003

930 bp DNA

BD144616

Novel G-protein coupled receptors.

BD144616

BD144616.1 GI:27850374

JP 2002112793-A/341.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 930)

Haga, T., Takeda, S. and Miyake, N.

Novel G-protein coupled receptors

Patent: JP 2002112793-A 341 16-APR-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002112793-A/341

PD 16-APR-2002

PF 09-FEB-2001 JP 2001034434

PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE

PC

C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K45/00, PC

A61K48/00,

A61P43/00, C07K14/705, C07K19/00, C12N1/15, C12N1/19, PC

C12N1/21,

C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/53, PC

C12N3/566//

C12P21/08, C12N15/00, A61K37/02, C12N5/00

Novel G-protein coupled receptors

Key Location/Qualifiers

(1) . . (930) .

CDS Location/Qualifiers

1. . 930

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

Query Matr. 100.0%; Score 930; DB 6; Length 930;

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Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACCTTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
DB 1 ATGATAACCTTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

QY 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAG 120
DB 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAG 120

QY 121 ATCTCCTTTTGTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG 180
DB 121 ATCTCCTTTTGTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG 180

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DB 241 AGAATCTGCTTATAATATCTGGGAGTGATCAACCATTTTCAGCACTGGCTTGTACT 300

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DB 301 ACCCTCAGCATATTTTATTGTTGCTCAAGATTTGCCAATTTCTCCAACTTTATTTTCTTCAC 360

QY 361 TTAAGAGGAGAGTTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTTTG 420
DB 361 TTAAGAGGAGAGTTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTTTG 420

QY 421 GCTTGTCACTTTTGTGATAAATCAATGATGATGTTGCGGACAAAGAAATTTGAGGA 480
DB 421 GCTTGTCACTTTTGTGATAAATCAATGATGATGTTGCGGACAAAGAAATTTGAGGA 480

QY 481 AACATGACTTGAAGAGTCAAAATTTGAAGAGTGCAATGTACTTTTCAAATATGACTGTAACC 540
DB 481 AACATGACTTGAAGAGTCAAAATTTGAAGAGTGCAATGTACTTTTCAAATATGACTGTAACC 540

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DB 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTGTAATCTGT 600

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DB 601 TCTTTGTGTAAACATCTCAAGAGATGCGAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660

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DB 901 GTGAAAGGAGAGAGACTTTCATCTCCATAG 930
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LOCUS AY114089 930 bp DNA linear PRI 28-FEB-2003
DEFINITION Homo sapiens putative taste receptor T2R52 gene, complete cds.
ACCESSION AY114089
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VERSION Y114089.1 GI:28603627
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Taxonomy: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Hominoidea; Hominidae; Homo.
REFERENCE 1 (bases 1 to 930)
AUTHORS Conte,C., Ebeling,M., Marcuz,A., Nef,P. and Andres-Barquin,P.J.
TITLE Identification and characterization of human taste receptor genes
belonging to the TAS2R family
JOURNAL Cytogenet. Genome Res. 98 (1), 45-53 (2002)
PUBMED 12584440
REFERENCE 2 (bases 1 to 930)
AUTHORS Conte,C., Ebeling,M., Marcuz,A., Nef,P. and Andres-Barquin,P.J.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Pharma Research Basel, F. Hoffmann-La Roche
Ltd., Grenzacherstrasse 124, Basel CH-4070, Switzerland
FEATURES
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Location/Qualifiers
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db_xref="taxon:9606"
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db_xref="GI:28603628"
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DQILPALAVSRVGLLWLLLNWYSTVLPAPNSVEVRTAYINAVIHFSNWLATTL
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NMTWKILKSAMYSNMTVTAVANLPFTLLSFMLLICSLCKLKKMKVHGKGSQD
PSTKVHIALQTVISFLLICAIYFLISIMISVMSFGSLENKPVFMFCKAIRFSYPSIHP
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mRNA
CDS
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ORIGIN

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Query Match 100.0%; Score 930; DB 8; Length 930;
Best Local Similarity 100.0%; Pred. No. 5.1e-181;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACCTTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
DB 1 ATGATAACCTTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

QY 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAG 120
DB 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAG 120

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QY 301 ACCCTCAGCATATTTTATTGTTGCTCAAGATTTGCCAATTTCTCCAACTTTATTTTCTTCAC 360
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AC018743_2 200001 310000
AC018743_3 300001 410000
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LOCUS AC018743 466818 bp DNA linear HTG 17-JUN-2003
DEFINITION Homo sapiens chromosome 12 clone RP11-289M22, WORKING DRAFT
ACCESSION AC018743
VERSION AC018743.27 GI:31791062
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

1 (bases 1 to 466818)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
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Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louissegh, H.,
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Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
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Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
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Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
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Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 466818)
Worley, K.C.

Direct Submission
Submitted (18-DEC-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 466818)
Worley, K.C.

Direct Submission
Submitted (17-JUN-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 17, 2003 this sequence version replaced gi:21431021.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMDC
Center clone name: RP11-289M22
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; version 0.990329
Assembly program: Phrap; version 100% of reads
Consensus quality: 463747 bases at least Q40
Consensus quality: 482989 bases at least Q30
Consensus quality: 494710 bases at least Q20
Estimated insert size: 386266; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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243154 243253: gap of unknown length
243254 269033: contig of 25780 bp in length

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Haves, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollings, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Humen, J., Joshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Liu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheeshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenko, S., Ogih, M., Okwuonu, G., Oreguay, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, J.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoohtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstein, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 167868)
Worley, K.C.
Direct Submission
Submitted (15-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 167868)
Worley, K.C.
Direct Submission
Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 167868)
Worley, K.C.
Direct Submission
Submitted (30-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 167868)
Worley, K.C.
Direct Submission
Submitted (24-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 167868)
Worley, K.C.
Direct Submission
Submitted (15-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 30, 2002 this sequence version replaced gi:22450371.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.
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| AUTHORS | 1 (bases 1 to 930) | | |
| TITLE | Fischer,A., Gilad,Y., Man,O. and Paabo,S. | | |
| JOURNAL | Evolution of Bitter Taste Receptors in Humans and Apes | | |
| PUBMED | Mol. Biol. Evol. 22 (3), 432-436 (2005) | | |
| REFERENCE | 15496549 | | |
| AUTHORS | 2 (bases 1 to 930) | | |
| TITLE | Anne,F., Yoav,G., Orna,M. and Svante,P. | | |
| JOURNAL | Direct Submission | | |
| FEATURES | Submitted (12-AUG-2004) Genetics, Max-Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany | | |
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ACCESSION AF494237.1 GI:20336530
VERSION
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SOURCE Homo sapiens (human)
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Hominoidea; Homo.
REFERENCE 1 (bases 1 to 930)
AUTHORS Bufo, B., Hofmann, T., Krautwurst, D., Ragnae, J.-D. and Meyerhof, W.
TITLE The human TAS2R16 receptor mediates bitter taste in response to
beta-glucopyranosides
JOURNAL Nat. Genet. 32 (3), 397-401 (2002)
PUBMED 12379855
REFERENCE 2 (bases 1 to 930)
AUTHORS Bufo, B., Hofmann, T., Krautwurst, D., Ragnae, J.-D. and Meyerhof, W.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2002) Molecular Genetics, German Institute of
Human Nutrition, Arthur-Scheunert Allee 114-116, Potsdam-Rehbrücke
14558, Germany
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DEFINITION Sequence 10 from Patent WO2004029087.
ACCESSION CQ800006
VERSION CQ800006.1 GI:46848948
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Bufo, B., Hofmann, T., Krautwurst, D., Kuhn, C. and Meyerhof, W.
TITLE Bitter taste receptors
JOURNAL Patent: WO 2004029087-A 10 08-APR-2004;
DEUTSCHES INSTITUT FUER ERNAHRUNGSFORSCHUNG (DE)
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| AUTHORS | Fischer, A., Gilad, Y., Mar, O. and Paabo, S. | | | | |
| TITLE | Evolution of Bitter Taste Receptors in Humans and Apes | | | | |
| JOURNAL | Mol. Biol. Evol. 22 (3), 432-436 (2005) | | | | |
| PUBMED | 15496549 | | | | |
| REFERENCE | 2 (bases 1 to 930) | | | | |
| AUTHORS | Anne, F., Yoav, G., Orna, N. and Svante, P. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (12-AUG-2004) Genetics, Max-Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany | | | | |
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| ORIGIN | Query Match 98.6%; Score 917.2; DB 8; Length 930; Best Local Similarity 99.1%; Pred. No. 2.e-178; Matches 922; Conservative 0; Mismatches 8; Indels 0; Gaps 0; | | | | |
| Qy | 1 ATGATACTTTTCTACCCATCATTTTTCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60 | | | | |
| Db | 1 ATGATACTTTTCTACCCATCATTTTTCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60 | | | | |
| Qy | 61 AATTTTGTAAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAAG 120 | | | | |
| Db | 61 AATTTTGTAAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAAG 120 | | | | |
| Qy | 121 ATCTCTTTGCTGACCAAAATTTCTCACTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180 | | | | |
| Db | 121 ATCTCTTTGCTGACCAAAATTTCTCACTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180 | | | | |
| Qy | 181 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240 | | | | |
| Db | 181 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240 | | | | |
| Qy | 241 AGAATCTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTCTACT 300 | | | | |
| Db | 241 AGAATCTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTCTACT 300 | | | | |
| Qy | 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAATTTATTTTCTTCAC 360 | | | | |
| Db | 301 AGCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCCAATTTATTTTCTTCAC 360 | | | | |
| Qy | 361 TTAAGAGAGAGATTAAGAGTGTCAATCTGTTGATGTTGTTGGGGCTTTTGTATTTTGG 420 | | | | |
| Db | 361 TTAAGAGAGAGATTAAGAGTGTCAATCTGTTGATGTTGTTGGGGCTTTTGTATTTTGG 420 | | | | |

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QY 421 GCTTGTCTATCTTTTGTGATAAACAATGAGATGAGATGTCGGGACAAAAGAAATTTGAAGA 480
Db 421 GCTTGTCTATCTTTTGTGATAAACAATGAGATGAGATGTCGGGACAAAAGAAATTTGAAGA 480
QY 481 AACATGACTTGAAGATCAAAATGAAGAGTGAATGACTCTTTTCAAAATGACTGTAACC 540
Db 481 AACATGACTTGAAGATCAAAATGAAGAGTGAATGACTCTTTTCAAAATGACTGTAACC 540
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTGGCTGTTAATCTGT 600
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QY 601 TCTTTGTGTAACATCTCAAGAGATGCGAGCTCCATGCTGATCTCTCTCTGTTATGTCGCAAT 660
Db 601 TCTTTGTGTAACATCTCAAGAGATGCGAGCTCCATGCTGATCTCTCTCTGTTATGTCGCAAT 660
QY 661 ACCAAGGTCACATAAAGCTTTGCAAACTGATGATCTCTCTCTGTTATGTCGCAAT 720
Db 661 ACCAAGGTCACATAAAGCTTTGCAAACTGATGATCTCTCTCTGTTATGTCGCAAT 720
QY 721 TACTTTCTGTCATATGATATCAGTTTGGAGTCTTTTGGAAAGTCTGGAAAACAAACCTGTC 780
Db 721 TACTTTCTGTCATATGATATCAGTTTGGAGTCTTTTGGAGTCTGGAAAACAAACCTGTC 780
QY 781 TTCTATGTTCTGCAAGCTATTAGATTCAGTATCTCTTCAATCCACCCATTCATCTGATT 840
Db 781 TTCTATGTTCTGCAAGCTATTAGATTCAGTATCTCTTCAATCCACCCATTCATCTGATT 840
QY 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTTTGGCAATGAGGTACTGG 900
Db 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTTTGGCAATGAGGTACTGG 900
QY 901 GTGAAGGAGAGAAGACTTTCATCTCCATAG 930
Db 901 GTGAAGGAGAGAAGACTTTCATCTCCATAG 930

RESULT 11
AY677147
LOCUS Pan paniscus taste receptor T2R43 (TAS2R) gene, complete cds.
DEFINITION Pan paniscus taste receptor T2R43 (TAS2R) gene, complete cds.
ACCESSION AY677147
VERSION AY677147.1 GI:54111484
KEYWORDS
SOURCE Pan paniscus (pygmy chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE
1 (bases 1 to 930)
Parry,C.M., Erkner,A. and le Coutre,J.
Divergence of T2R chemosensory receptor families in humans,
bonobos, and chimpanzees
Proc. Natl. Acad. Sci. U.S.A. 101, 14830-14834 (2004)
15466715
JOURNAL
PUBMED
2 (bases 1 to 930)
Parry,C.M., Erkner,A. and le Coutre,J.
Direct Submission
AUTHORS
Submitted (05-JUL-2004) Nestle Research Centre, P.O. Box 44,
CH-1000 Lausanne 26 1000, Switzerland
FEATURES
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ORIGIN

Query Match 98.4%; Score 915.2; DB 8; Length 930;
Best Local Similarity 99.1%; Pred. No. 5.6e-178;
Matches 920; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGATAAATTTTACCCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTTCTTATTGA 60
Db 1 ATGATAAATTTTACCCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTTCTTATTGA 60
QY 61 AATTTGTAAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGAGACAAAAG 120
Db 61 AATTTGTAAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGAGACAAAAG 120
QY 121 ATCTCTTGTGACCAAAATTCACCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 121 ATCTCTTGTGACCAAAATTCACCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
QY 181 GTATTATTATAAATCGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 181 GTATTATTATAAATCGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
QY 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACATTTCAAGCACTGGCTGCTACT 300
Db 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACATTTCAAGCACTGGCTGCTACT 300
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCAACTTTATTTTCTTCCAC 360
Db 301 AGCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCAACTTTATTTTCTTCCAC 360
QY 361 TTAAGAGGAGAGTAAAGAGTGTCTTCTGTTGATGTTGTTGGGCGCTTTTGTCTATTGTTG 420
Db 361 TTAAGAGGAGAGTAAAGAGTGTCTTCTGTTGATGTTGTTGGGCGCTTTTGTCTATTGTTG 420
QY 421 GCTTGTCTATCTTTTGTGATAAACAATGAGATGAGTGTGCGGACAAAAGAAATTTGAAGA 480
Db 421 GCTTGTCTATCTTTTATGATAAACAATGAGATGAGTGTGCGGACAAAAGAAATTTGAAGA 480
QY 481 AACATGACTTGAAGATCAAAATGAAGAGTGAATGACTCTTTTCAAAATGACTGTAACC 540
Db 481 AACATGACTTGAAGATCAAAATGAAGAGTGAATGACTCTTTTCAAAATGACTGTAACC 540
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
Db 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
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Db 601 TCTTTGTGTAACATCTCAAGAGATGCGAGCTCCATGCTGATCTCTCTCTGTTATGTCGCAAT 660
QY 661 ACCAAGGTCACATAAAGCTTTGCAAACTGATGATCTCTCTCTGTTATGTCGCAAT 720
Db 661 ACCAAGGTCACATAAAGCTTTGCAAACTGATGATCTCTCTCTGTTATGTCGCAAT 720
QY 721 TACTTTCTGTCATATGATATCAGTTTGGAGTCTTTTGGAAAGTCTGGAAAACAAACCTGTC 780
Db 721 TACTTTCTGTCATATGATATCAGTTTGGAGTCTTTTGGAGTCTGGAAAACAAACCTGTC 780
QY 781 TTCTATGTTCTGCAAGCTATTAGATTCAGTATCTCTTCAATCCACCCATTCATCTGATT 840
Db 781 TTCTATGTTCTGCAAGCTATTAGATTCAGTATCTCTTCAATCCACCCATTCATCTGATT 840
QY 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTTTGGCAATGAGGTACTGG 900
Db 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTTTGGCAATGAGGTACTGG 900
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ORIGIN
Query Match          92.9%; Score 863.6; DB 8; Length 870;
Best Local Similarity 99.5%; Pred. No. 2.3e-167;
Matches 866; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 28 TCCAGTCGTGAGTGGTACATTTGTTATTTGGAATTTTCTTAATGGCTTCATAGCACTG 87
DB 1 TCCAGTCGTGAGTGGTACATTTGTTATTTGGAATTTTCTTAATGGCTTCATAGCACTG 60

QY 88 GTAAATTCATTCAGTGGTTCAGAGACAAAGATCTCTTGTGCTGACCAAAATTCCTACT 147
DB 61 GTAAATTCATTCAGTGGTTCAGAGACAAAGATCTCTTGTGCTGACCAAAATTCCTACT 120

QY 148 GCTCTGGCGGCTCCAGAGTGGTGTCTGGGTATTAATTAATAAATTCGTTCAACT 207
DB 121 GCTCTGGCGGCTCCAGAGTGGTGTCTGGGTATTAATTAATAAATTCGTTCAACT 180

QY 208 GTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACCTGCTTAATAATCTGGCA 267
DB 181 GTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACCTGCTTAATAATCTGGCA 240

QY 268 GTGATCAACCAATTCAGCAACTGGCTTGCTACTACCTCAGCATATTTATTTGCTCAAG 327
DB 241 GTAATCAACCAATTCAGCAACTGGCTTGCTACTACCTCAGCATATTTATTTGCTCAAG 300

QY 328 ATTGCAATTCCTCAACTTTATTTTCTCACTTAAGAGAGAGAGTTAAGAGTGTCAAT 387
DB 301 ATTGCAATTCCTCAACTTTATTTTCTCACTTAAGAGAGAGAGTTAAGAGTGTCAAT 360

QY 388 CTGGTGATGTTCTGGGGCTTTGCTATTTTGGCTTGCTATCTTTTGTGATAACATG 447
DB 361 CTGGTGATGTTCTGGGGCTTTGCTATTTTGGCTTGCTATCTTTTGTGATAACATG 420

QY 448 AATGAGATTGTCGGACAAAAGAAATTTGAAGAAAACATGACTTGAAGATCAAAATGAAG 507
DB 421 AATGAGATTGTCGGACAAAAGAAATTTGAAGAAAACATGACTTGAAGATCAAAATGAAG 480

QY 508 AGTCAATGATCTTTTCAAAATGATCTGPAACCATGGTAGCAAACTTAGTACCTTCACT 567
DB 481 AGTCAATGATCTTTTCAAAATGATCTGPAACCATGGTAGCAAACTTAGTACCTTCACT 540

QY 568 CTGACCTACTATCTTTTATGCTGTGTAATCTGTTTGTGTGTAACATCTCAAGAGATG 627
DB 541 CTGACCTACTATCTTTTATGCTGTGTAATCTGTTTGTGTGTAACATCTCAAGAGATG 600

QY 628 CAGCTCCATGGTAAAGGATCTCAAGATCCAGACCAAGGTCACATAAAGCTTTGCAA 687
DB 601 CAGCTCCATGGTAAAGGATCTCAAGATCCAGACCAAGGTCACATAAAGCTTTGCAA 660
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QY 688 ACTGTGATCTCTCTCTCTCTGTTATGTGCAATTAATTTCTGTCATTAATGATATCAGTT 747
DB 661 ACTGTGATCTCTCTCTCTCTGTTATGTGCAATTAATTTCTGTCATTAATGATATCAGTT 720

QY 748 TGGAGTGTGGAGTCTGGAACAAACCTGCTTCATGTTCTGCAAGCTATTAGATTC 807
DB 721 TGGAGTGTGGAGTCTGGAACAAACCTGCTTCATGTTCTGCAAGCTATTAGATTC 780

QY 808 AGCTATCTCTCAATCACCACCTTCATCTCTGATTTGGGAAAAACAAGAGCTAAAGCAGACT 867
DB 781 AGCTATCTCTCAATCACCACCTTCATCTCTGATTTGGGAAAAACAAGAGCTAAAGCAGACT 840

QY 868 TTTCTTTCAGTTTTTTGGCAATGAGGTAC 897
DB 841 TTTCTTTCAGTTTTTTGGCAATGAGGTAC 870

RESULT 14
AY724878          930 bp DNA linear PRI 17-FEB-2005
LOCUS             Pan troglodytes chromosome 12 taste receptor T2R44 gene, complete
DEFINITION        cds.
ACCESSION          AY724878
VERSION            AY724878.1 GI:51989080
KEYWORDS            Pan troglodytes (chimpanzee)
SOURCE             Pan troglodytes
ORGANISM            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                    Homnidae; Pan.
REFERENCE           1 (bases 1 to 930)
AUTHORS             Fischer,A., Gilad,Y., Man,O. and Paabo,S.
TITLE               Evolution of Bitter Taste Receptors in Humans and Apes
JOURNAL             Mol. Biol. Evol. 22 (3), 432-436 (2005)
PUBMED             15496549
REFERENCE           2 (bases 1 to 930)
AUTHORS             Anne,F., Yoav,G., Orna,M. and Svante,P.
TITLE               Direct Submission
JOURNAL             Submitted (12-AUG-2004) Genetics, Max-Planck Institute for
                    Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,
                    Germany
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                     NFKLSAVLSYDATTVTGTLNLPFTLLCLLCSLCHLKKQQLHGGSDQ
                     PSTKVHIKQTVISFLLCALYIFLUSIMISVWSFSLNKPVMFKAIRFSYPSIHP
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CDS
Query Match          92.6%; Score 861.2; DB 8; Length 930;
Best Local Similarity 95.4%; Pred. No. 7.1e-167;
Matches 887; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGTAACCTTTTCTACCCATCATTTTTCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
DB 1 ATGCAACTTTTATACCCATTAATTTTTCAGTCTGGTAGTGGTTATTATTGTTATTGGA 60

QY 61 AATTTTGTAAATGGCTTCATAGCACTGGTAATATTCATTTGAGTGGTTCAGAGACAAAAG 120
DB 61 AATTTTGTAAATGGCTTCATAGCACTGGTAATATTCATTTGAGTGGTTCAGAGACAAAAG 120

QY 121 ATCTCTTTGCTGACCAAAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
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| | | | |
|----|-----|--|-----|
| Db | 121 | ATCTCTTTTGTGACCAAAATTCACCTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTCTGG | 180 |
| Qy | 181 | GTATTATTATTAAATCGGTATTCACCTGTGTGGAATCCAGCTTTTAAATAGTGTAGAAGTA | 240 |
| Db | 181 | GTATTATTATTAAATCGGTATTCACCTGTGTGGAATCCAGCTTTTAAATAGTGTAGAAGTA | 240 |
| Qy | 241 | AGAACTACTGCTTATAATATCTGGCAGTGATCAACCAATTCAGCAACTGGCTGCTACT | 300 |
| Db | 241 | AGAACTACTGCTTATAATATCTGGCAGTGATCAACCAATTCAGCAACTGGCTGCTACT | 300 |
| Qy | 301 | ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCCAACTTTTATTTTCTTCTCAC | 360 |
| Db | 301 | ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCCAACTTTTATTTTCTTCTCAC | 360 |
| Qy | 361 | TTAAAGAGGAGATTTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTTTGG | 420 |
| Db | 361 | TTAAAGAGGAGATTTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTTACTATTTTGG | 420 |
| Qy | 421 | GCTTGTCTATCTTTTGTGATTAACATGAATGAGATTGTGCGGACAAAGATTTTGAAGGA | 480 |
| Db | 421 | GCTTGTCTATCTTTTGTGATTAACATGAATGAGATTGTGCGGACAAAGATTTTGAAGGA | 480 |
| Qy | 481 | AACATGACTTGAAGATCAAAATTTGAAGAGTGCATGCTATTTTCAAAATATGACTGTAAACC | 540 |
| Db | 481 | AACATGACTTGAAGATCAAAATTTGAAGAGTGCATGCTATTTTCAAAATATGACTGTAAACC | 540 |
| Qy | 541 | ATGGTAGCAAACTTAGTACCTTCTACTCTGACCTACTATCTTTTATGCTGTGTAATCTGT | 600 |
| Db | 541 | ACGCTAGGAAACTTAGTACCTTCTACTCTGACCTACTATGTTTGTGTTGCTGTAAATCTGT | 600 |
| Qy | 601 | TCCTTTGTGTAACATCTCAAGAGATGCACTGCTCCATGTTGTAAGGATCTCAAGATCCCAGC | 660 |
| Db | 601 | TCCTGTGTAAACATCTCAAGAGATGCACTGCTCCATGTTGTAAGGATCTCAAGATCCCAGC | 660 |
| Qy | 661 | ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTCTTGTATGTGCCATT | 720 |
| Db | 661 | ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTCTTGTATGTGCCATT | 720 |
| Qy | 721 | TACTTTCTGTCATTAATGATATCAGTTTGGAGTGTGGAAGTCTGGAAACAAACCTGTCT | 780 |
| Db | 721 | TACTTTCTGTCATTAATGATATCAGTTTGGAGTGTGGAAGTCTGAAACAAACCTGTCT | 780 |
| Qy | 781 | TTCTATGTTCTGCAAGCTATTAGATTACGATCTCTCAATCCACCTTCACTCTGATT | 840 |
| Db | 781 | TTCTATGTTCTGCAAGCTATTAGATTACGATCTCTCAATCCACCTTCACTCTGATT | 840 |
| Qy | 841 | TGGGGAACAAGAAGCTAAAGCAGACTTTTCTTTCAGTTTTTGGCAATGAGGTACTGG | 900 |
| Db | 841 | TGGGGAACAAGAAGCTAAAGCAGACTTTTCTTTCAGTTTTTGGCGCAAGTGAGGTACTGG | 900 |
| Qy | 901 | GTGAAAGGAGAGAAGCTTCATCTCCATAG | 930 |
| Db | 901 | GTGAAAGGAGAGAAGCTTCATCTCCATAG | 930 |

RESULT 15
LOCUS AY677148 930 bp DNA linear PRI 18-OCT-2004
DEFINITION Pan paniscus taste receptor T2R44 (TAS2R) gene, complete cds.
ACCESSION AY677148
VERSION AY677148.1 GI:54111486
KEYWORDS Pan paniscus (pygmy chimpanzee)
SOURCE Pan paniscus
ORGANISM Pan paniscus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
1 (bases 1 to 930)
REFERENCE Parry,C.M., Erkner,A. and le Coutre,J.
AUTHORS Divergence of T2R chemosensory receptor families in humans,
TITLE bonobos, and chimpanzees
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101, 14830-14834 (2004)

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| 15466715 | PUBMED | 2 (bases 1 to 930) | 180 |
| Parry,C.M., Erkner,A. and le Coutre,J. | REFERENCE | Direct Submission | 240 |
| Submitted (05-JUL-2004) Nestle Research Centre, P.O. Box 44, | AUTHORS | Location/Qualifiers | 240 |
| CH-1000 Lausanne 26 1000, Switzerland | JOURNAL | 1..930 | 300 |
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| | | 1..930 | 840 |
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| | | SIFYLKILRNFNLIFLHKKRVKSVILVLLGFLPLFLACQLFMVIMKEIVRTKEYEG | 930 |
| | | NMTWKILRSAYVLSDATVTTGLNLPFTLLCFLLICSLCKHLKQWHLGKGSQD | 930 |
| | | PSTKVHLVQTVISFLLLCAIYELISVMSFGLSKNKPVPFMECKAIRPSYPSIHP | 930 |
| | | FILWGNKQKQTLFSLVRQVRYWVKGKPSSP" | 930 |
| | ORIGIN | | |
| | Query Match | 92.4%; Score 859.2; DB 8; Length 930; | |
| | Best Local Similarity | 95.4%; Pred. No. 1.8e-166; | |
| | Matches | 885; Conservative 0; Mismatches 43; Indels 0; Gaps 0; | |
| Qy | 1 | ATGATAAATTTTACCAATCATTTTTCAGTCTGTGAGTGTGTACATTTGTTATTGGA | 60 |
| Db | 1 | ATGATAAATTTTATATACCAATCATTTTTCAGTCTGTGAGTGTGTATTTTATTGGA | 60 |
| Qy | 61 | AATTTTGTATGAGTCTCATAGCACTGTAATTCATTTGAGTGTGTCAAGAGACAAAG | 120 |
| Db | 61 | AATTTTGTATGAGTCTCATAGCACTGTAATTCATTTGAGTGTGTCAAGAGACAAAG | 120 |
| Qy | 121 | ATCTCTTTGTGACCAAAATTCCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG | 180 |
| Db | 121 | ATCTCTTTGTGACCAAAATTCCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG | 180 |
| Qy | 181 | GTATTATTATTAACTGCTATTCAACTGTGTGGAATCCAGCTTTTAAATAGTGTAGAAGTA | 240 |
| Db | 181 | GTATTATTATTAAATTTGATTTCACTGTGTGGAATCCAGCTTTTATAGTGTAGAAGTA | 240 |
| Qy | 241 | AGAACTACTGCTTATAATATCTGGCAGTGATCAACCAATTTTCAGCAACTGGCTGCTACT | 300 |
| Db | 241 | AGAACTACTGCTTATAATATCTGGCAGTGATCAACCGGCCATTTTCAGCAACTGGCTGCTACT | 300 |
| Qy | 301 | ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTTCTCCAACTTTTATTTTCTTCTCAC | 360 |
| Db | 301 | AGCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTTCTCCAACTTTTATTTTCTTCTCAC | 360 |
| Qy | 361 | TTAAAGAGGAGATTTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTGCTATTTTGG | 420 |
| Db | 361 | TTAAAGAGGAGATTTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTTACTATTTTGG | 420 |
| Qy | 421 | GCTTGTCTATCTTTTGTGATTAACATGAATGAGATTGTGCGGACAAAGAAATTTGAAGGA | 480 |
| Db | 421 | GCTTGTCTATCTTTTGTGATTAACATGAATGAGATTGTGCGGACAAAGAAATATGAAGGA | 480 |
| Qy | 481 | AACATGACTTGAAGATCAAAATTTGAAGAGTGCATGCTACTTTTCAAAATATGACTGTAAACC | 540 |
| Db | 481 | AACATGACTTGAAGATCAAAATTTGAAGAGTGCAGTGTACTTTTCAAGATGCGACTGTAAACC | 540 |
| Qy | 541 | ATGGTAGCAAACTTAGTACCTTCTACTCTGACCTACTATCTTTTATGCTGTGTAATCTGT | 600 |
| Db | 541 | ACGCTAGGAAACTTAGTACCTTCTACTCTGACCTACTATGTTTGTGTTGCTGTAAATCTGT | 600 |

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2006, 05:41:05 ; Search time 618 Seconds
(without alignments)
10029.392 Million cell updates/sec

Title: US-09-825-882-7
Perfect score: 930
Sequence: 1 atgataattttctaccat.....agaagacttcctccatag 930

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 930 | 100.0 | 930 | 6 | AAS18167 |
| 2 | 930 | 100.0 | 930 | 6 | ABZ43210 Human T2R |
| 3 | 930 | 100.0 | 930 | 8 | ABZ68712 Human GPC |
| 4 | 930 | 100.0 | 930 | 12 | ADI32659 Human tas |
| 5 | 930 | 100.0 | 930 | 13 | ADR29239 Taste rec |
| 6 | 930 | 100.0 | 1179 | 8 | ACC44478 Gene enco |
| 7 | 930 | 100.0 | 1330 | 10 | ADC87038 Human GPC |
| 8 | 924 | 99.4 | 930 | 14 | ADM74419 Human bit |
| 9 | 922.2 | 99.2 | 927 | 13 | ADM33296 Human bit |
| 10 | 852.8 | 91.7 | 930 | 14 | ADM74575 Human bit |
| 11 | 851.6 | 91.6 | 930 | 6 | AAS18169 Human T2R |
| 12 | 851.6 | 91.6 | 930 | 6 | ABZ43215 Human GPC |
| 13 | 851.6 | 91.6 | 930 | 8 | ACC44476 Gene enco |
| 14 | 851.6 | 91.6 | 930 | 13 | ADR29243 Taste rec |
| 15 | 851.6 | 91.6 | 971 | 10 | ADD18119 Human G-p |
| 16 | 851.6 | 91.6 | 1330 | 10 | ADC87040 Human GPC |
| 17 | 851.2 | 91.5 | 930 | 14 | ADM74581 Human bit |
| 18 | 850.4 | 91.4 | 930 | 14 | ADM74421 Human bit |
| 19 | 850.2 | 91.4 | 927 | 13 | ADM33298 Human bit |

| | | | | | |
|----|-------|------|------|----|--------------------|
| 20 | 849.6 | 91.4 | 930 | 14 | ADM74577 Human bit |
| 21 | 849.6 | 91.4 | 930 | 14 | ADM74583 Human bit |
| 22 | 848 | 91.2 | 930 | 14 | ADM74587 Human bit |
| 23 | 848 | 91.2 | 930 | 14 | ADM74585 Human bit |
| 24 | 848 | 91.2 | 930 | 14 | ADM74579 Human bit |
| 25 | 829.2 | 89.2 | 930 | 6 | AAS18173 Human T2R |
| 26 | 829.2 | 89.2 | 930 | 8 | ACC44475 Gene enco |
| 27 | 829.2 | 89.2 | 930 | 13 | ADR29251 Taste rec |
| 28 | 829.2 | 89.2 | 930 | 14 | ADM74595 Human bit |
| 29 | 829.2 | 89.2 | 1330 | 10 | ADC87130 Human GPC |
| 30 | 827.6 | 89.0 | 930 | 14 | ADM74597 Human bit |
| 31 | 827.6 | 89.0 | 930 | 14 | ADM74593 Human bit |
| 32 | 826 | 88.8 | 930 | 14 | ADM74589 Human bit |
| 33 | 824.4 | 88.6 | 930 | 14 | ADM74591 Human bit |
| 34 | 824.4 | 88.6 | 930 | 14 | ADM74599 Human bit |
| 35 | 822.8 | 88.5 | 1300 | 10 | ADC87026 Human GPC |
| 36 | 801.4 | 86.2 | 900 | 14 | ADM74423 Human bit |
| 37 | 801 | 86.1 | 897 | 13 | ADM33302 Human bit |
| 38 | 799.6 | 86.0 | 960 | 8 | ACC44470 Gene enco |
| 39 | 799.6 | 86.0 | 960 | 14 | ADM74603 Human bit |
| 40 | 799.6 | 86.0 | 1360 | 10 | ADC87028 Human GPC |
| 41 | 798 | 85.8 | 960 | 14 | ADM74607 Human bit |
| 42 | 798 | 85.8 | 960 | 14 | ADM74605 Human bit |
| 43 | 798 | 85.8 | 960 | 14 | ADM74601 Human bit |
| 44 | 797.6 | 85.8 | 929 | 14 | ADM74425 Human bit |
| 45 | 796.6 | 85.7 | 926 | 13 | ADM33304 Human bit |

ALIGNMENTS

RESULT 1
AAS18167
ID AAS18167 standard; cDNA; 930 BP.
XX
AC AAS18167;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human T2R61 (ht2R61) cDNA.
XX
KW Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor;
KW ht2R61; T2R61; T2R; bitter taste sensation; taste signalling pathway; ss;
KW taste transduction; food taste masking; drug taste masking.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..930
FT /*tag= a
FT /product= "Human T2R61"
XX
PN WO200177676-A1.
XX
PD 18-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010739.
XX
PR 07-APR-2000; 2000US-0195532P.
PR 13-NOV-2000; 2000US-0247014P.
XX
(SENO-) SENOMYX INC.
PI Adler JE;
DR WPI; 2002-017486/02.
P-PSDB; AAU11384.
XX
Novel isolated mammalian taste cell-specific G protein-coupled receptor,
T2R, involved in bitter taste sensation, useful for identifying taste
modulators that are used to decrease or mask bitter taste of foods or
drugs.

Db 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAGAGACAAAAG 120
QY 121 ATCTCCTTTGCTGACCAAAATCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTCTGG 180
Db 121 ATCTCCTTTGCTGACCAAAATCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTCTGG 180
QY 181 GTATTATTATAAATCTGGTATTCACACTGTTGTAATCCAGCTTTTAATAGTGTAGAGTA 240
Db 181 GTATTATTATAAATCTGGTATTCACACTGTTGTAATCCAGCTTTTAATAGTGTAGAGTA 240
QY 241 AGAACTACTGCTTATATAATATCTGGGCAAGTATCAACCAATTCAGCAACTGGCTTGTCTACT 300
Db 241 AGAACTACTGCTTATATAATATCTGGGCAAGTATCAACCAATTCAGCAACTGGCTTGTCTACT 300
QY 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACCTTTATTTTCTTCCAC 360
Db 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACCTTTATTTTCTTCCAC 360
QY 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTGAATGTTGTTGGGCTTTGCTATTTTGG 420
Db 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTGAATGTTGTTGGGCTTTGCTATTTTGG 420
QY 421 GCTTGTCTATCTTTTGTGATAAATGATGATTTGTCGCAAAAGAAATTTGAAGGA 480
Db 421 GCTTGTCTATCTTTTGTGATAAATGATGATTTGTCGCAAAAGAAATTTGAAGGA 480
QY 481 AACATGACTTGAAGATCAAAATTTGAAGAGTGAATGTAATTTTCAAAATATGACTGTAAAC 540
Db 481 AACATGACTTGAAGATCAAAATTTGAAGAGTGAATGTAATTTTCAAAATATGACTGTAAAC 540
QY 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCTCACTAATCTTTTATGCTGTAAATCTGT 600
Db 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCTCACTAATCTTTTATGCTGTAAATCTGT 600
QY 601 TCTTTGTGTAAACATCTCAAGAGATGCACTCCATGTTAAAGGATCTCAAGATCCGAC 660
Db 601 TCTTTGTGTAAACATCTCAAGAGATGCACTCCATGTTAAAGGATCTCAAGATCCGAC 660
QY 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCCATT 720
Db 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCCATT 720
QY 721 TACTTTCTGTCATATATGATATCAGTTGGAGTTTGGAGTCTCGAATAAACAACCTGTC 780
Db 721 TACTTTCTGTCATATATGATATCAGTTGGAGTTTGGAGTCTCGAATAAACAACCTGTC 780
QY 781 TTTCTGTTCTGCAAAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCATCTGATT 840
Db 781 TTTCTGTTCTGCAAAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCATCTGATT 840
QY 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTTTCAGTTTTTTTGGCAATGAGGTACTGG 900
Db 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTTTCAGTTTTTTTGGCAATGAGGTACTGG 900
QY 901 GTGAAGAGAGAGAGACTTCATCTCCATAG 930
Db 901 GTGAAGAGAGAGAGACTTCATCTCCATAG 930

RESULT 3

ABZ68712
ID ABZ68712 standard; DNA; 930 BP.
AC ABZ68712;
XX
XX
XX
XX 16-MAY-2003 (first entry)
XX Nucleotide sequence of human T2R61 polypeptide.
DE Human; T2R4; G protein coupled receptor; GPCR; taste receptor;
KW bitter alkaloid quinine; denatonium; 6-nitrosaccharin; T2R44; T2R61;
KW bitter taste; saccharin; Gene; ss.
XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..930

FT /*tag= a

XX /product= "T2R61"

PN WO2003006482-A2.

XX 23-JAN-2003.

XX 10-JUL-2002; 2002WO-US021602.

XX 10-JUL-2001; 2001US-0303811P.

PR 15-APR-2002; 2002US-0372089P.

XX (SENO-) SENOMYX INC.

XX Pronin A, Connor J, Tang H, Keung W, Servant G, Adler JB;

PI O'Connell S, Brust P;

XX WPI; 2003-221711/21.

DR P-PSDB; ABP97669.

XX Assay method for identifying a compound, which modulates hT2R4 associated bitter taste, involves screening a compound for its effect on quinine or a structurally related compound to induce activation of hT2R4.

PS Disclosure; Page 11-12; 82pp; English.

XX The present sequence encodes a human T2R61 protein. T2R61 is a G protein coupled receptor (GPCR) that is specifically activated by the bitter derivative of saccharin, 6-nitrosaccharin. T244 is activated by denatonium and 6-nitrosaccharin. T2R4 is activated by the bitter alkaloid quinine. The specification describes an assay for identifying compounds which modulate T2R4, T2R61 and T2R44 associated bitter taste. The identified compounds are used in foods, beverages and medicines to inhibit bitter taste e.g. saccharin containing diet beverages, foods or medicinal products

SQ Sequence 930 BP; 255 A; 177 C; 179 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 930; DB 8; Length 930;

Best Local Similarity 100.0%; Pred. No. 1.2e-247;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTTCACCATCATTTTTCAGTCTGTTTCCAGTCTGTTTGTATTTGTTATTCGA 60

Db 1 ATGATAACTTTTTCACCATCATTTTTCAGTCTGTTTCCAGTCTGTTTGTATTTGTTATTCGA 60

QY 61 AATTTTGTCTAATGCTTCATAGCACTGGTAAATTCATTTCCAGTCTGTTTCAAGAGACAAAAG 120

Db 61 AATTTTGTCTAATGCTTCATAGCACTGGTAAATTCATTTCCAGTCTGTTTCAAGAGACAAAAG 120

QY 121 ATCTCCTTTGCTGACCAAAATTCCTCACTGCTCTGCGGCTCTCCAGAGTTGGTTTGTCTGG 180

Db 121 ATCTCCTTTGCTGACCAAAATTCCTCACTGCTCTGCGGCTCTCCAGAGTTGGTTTGTCTGG 180

QY 181 GTATTATTATAAATCTGGTATTCAACTGTTGTTGAATCCAGCTTTTAATAGTGTAGAGTA 240

Db 181 GTATTATTATAAATCTGGTATTCAACTGTTGTTGAATCCAGCTTTTAATAGTGTAGAGTA 240

QY 241 AGAACTACTGCTTATAATATCTGGGCAAGTATCAACCAATTCAGCAACTGGCTTGTCTACT 300

Db 241 AGAACTACTGCTTATAATATCTGGGCAAGTATCAACCAATTCAGCAACTGGCTTGTCTACT 300

QY 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACCTTTATTTTCTTCCAC 360

Db 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCCAACCTTTATTTTCTTCCAC 360

QY 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTGAATGTTGTTGGGCTTTGCTATTTTGG 420

Db 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGGTGAATGTTGTTGGGCTTTGCTATTTTGG 420

```
QY 421 GCTTGTCTATCTTTTGTGATAAACAATGATGAGATTGTGCGACAAAAGAAATTTGAAGA 480
Db 421 GCTTGTCTATCTTTTGTGATAAACAATGATGAGATTGTGCGACAAAAGAAATTTGAAGA 480
QY 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGCATGTACTTTTCAAAATATGACTCTAAC 540
Db 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGCATGTACTTTTCAAAATATGACTCTAAC 540
QY 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGT 600
Db 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGT 600
QY 601 TCTTTGTGTAAACATCTCAAGAGATGCGAGCTCCATGGTAAAGGATCTCAAGATCCGAG 660
Db 601 TCTTTGTGTAAACATCTCAAGAGATGCGAGCTCCATGGTAAAGGATCTCAAGATCCGAG 660
QY 661 ACCAAGGTCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCCATT 720
Db 661 ACCAAGGTCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCCATT 720
QY 721 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAAAGTCTCGAAAACAAACCTGTC 780
Db 721 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAAAGTCTCGAAAACAAACCTGTC 780
QY 781 TTTGATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCAGCTTCACTCTGATT 840
Db 781 TTTGATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCAGCTTCACTCTGATT 840
QY 841 TGGGGAACAAAGACTAAAGCAGACTTTTCTTTCAGTTTGTGGCAATGAGTACTGG 900
Db 841 TGGGGAACAAAGACTAAAGCAGACTTTTCTTTCAGTTTGTGGCAATGAGTACTGG 900
QY 901 GTGAAAGGAGAGAAGACTTTCATCTCCATAG 930
Db 901 GTGAAAGGAGAGAAGACTTTCATCTCCATAG 930
```

RESULT 4

AD132659
ID AD132659 standard; DNA; 930 BP.

XX
AC AD132659;

DT 22-APR-2004 (first entry)

XX Human taste receptor-related THTR9 DNA.

XX G protein-coupled receptor; GPCR; food processing; seasoning; human;
KW taste receptor; THTR9; db.

XX Homo sapiens.

OS
XX WO2004007716-A1.

PN
XX 22-JAN-2004.

PD
XX 17-JUL-2003; 2003WO-JP009093.

PF
XX 17-JUL-2002; 2002JP-00208284.

PR
XX (UYN1-) UNIV NIPPON.

PA Takao K, Suga H, Takao T;

XX WPI; 2004-122947/12.

XX Isolation of GPCR (G protein-coupled receptor) gene from human brain
PT tissue for constructing vector and transformant to produce THTR taste
PT receptor protein and screening its ligands for use in foods.

XX Claim 9; SEQ ID NO 1; 84pp; Japanese.

XX

CC The invention relates to a novel method for isolating a G protein-coupled
CC receptor (GPCR) gene comprising designing primers based on sequence data
CC for known GPCR genes and their surrounding domains, amplification with
CC the use of these primers and cDNA libraries from tissues other than those
CC expressing such genes, cloning the thus amplified fragment and
CC identifying the cloned gene. The GPCR gene of the invention and its
CC encoded protein may be applicable in screening for ligands that regulate
CC taste which may then be used in food compositions e.g. for seasoning and
CC food processing, as well as for providing a database for studying other
CC genes. The current sequence is that of the human taste receptor-related
CC THTR9 DNA of the invention.

XX
SQ Sequence 930 BP; 255 A; 177 C; 179 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 930; DB 12; Length 930;
Best Local Similarity 100.0%; Pred. No. 1.2e-247;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTACCCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

Db 1 ATGATAACTTTTACCCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60

QY 61 AATTTTGCTAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGAGACAAAAG 120

Db 61 AATTTTGCTAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGAGACAAAAG 120

QY 121 ATCTCCTTTGCTGACCAAAATTCCTACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180

Db 121 ATCTCCTTTGCTGACCAAAATTCCTACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180

QY 181 GTATTATTATTAACTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240

Db 181 GTATTATTATTAACTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240

QY 241 AGAAGTCTGCTTAAATATCTGGGCACTGATCAACATTTTCAGCACTGGCTTCTACT 300

Db 241 AGAAGTCTGCTTAAATATCTGGGCACTGATCAACATTTTCAGCACTGGCTTCTACT 300

QY 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCAACTTTTATTTTCTTCAC 360

Db 301 ACCCTCAGCATATTTTATTGCTCAAGATTCGCAATTTCTCAACTTTTATTTTCTTCAC 360

QY 361 TTAAAGAGGAGAGTTAAGAGTGTCAATCTGGTGTAGTGTGGGGCCCTTTGCTATTTTG 420

Db 361 TTAAAGAGGAGAGTTAAGAGTGTCAATCTGGTGTAGTGTGGGGCCCTTTGCTATTTTG 420

QY 421 GCTTGTCACTTTTGTGATAAAATGAATGAGATGTGCGGACAAAAGAAATTTGAAGA 480

Db 421 GCTTGTCACTTTTGTGATAAAATGAATGAGATGTGCGGACAAAAGAAATTTGAAGA 480

QY 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGCATTTTCAAAATATGACTGTAAAC 540

Db 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGCATTTTCAAAATATGACTGTAAAC 540

QY 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600

Db 541 ATGGTAGCAAACTTAGTACCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600

QY 601 TCTTTGTGTAAACATCTCAAGAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCCAGC 660

Db 601 TCTTTGTGTAAACATCTCAAGAGATGCAGCTCCATGGTAAAGGATCTCAAGATCCCAGC 660

QY 661 ACCAAGGTCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCCATT 720

Db 661 ACCAAGGTCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCCATT 720

QY 721 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAAAGTCTCGAAAACAAACCTGTC 780

Db 721 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAAAGTCTCGAAAACAAACCTGTC 780

QY 781 TTTGATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCAGCTTCACTCTGATT 840

Db 781 TTTGATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCAGCTTCACTCTGATT 840

QY 841 TGGGAAACAGAGAGCTAAGCAGACTTTCTTTTCAGTTTTTGGCAAAATGAGGTACTGG 900
DB 841 TGGGAAACAGAGAGCTAAGCAGACTTTCTTTTCAGTTTTTGGCAAAATGAGGTACTGG 900
QY 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930
DB 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930

RESULT 5
ID ADR29239 standard; DNA; 930 BP.
XX ADR29239; (first entry)
AC 04-NOV-2004 (first entry)
DT Taste receptor modulation-related human T2R61 gene sequence SeqID178.
DE T1R; T2R; taste receptor; G protein; modulatory compound; MAPK activity;
KW CAMP accumulation; adenylyl cyclase; bitter; taste; umami; sweet; T2R61;
KW gene; da; human.
XX Homo sapiens.
OS WO2004069191-A2.
PN 19-AUG-2004.
XX 03-FEB-2004; 2004WO-US002987.
XX 03-FEB-2003; 2003US-0444172P.
PR 26-MAR-2003; 2003US-0457318P.
XX (SENO-) SENOMYX INC.
XX Servant G, Ozeck M, Brust P, Xu H;
PI WPI; 2004-604341/58.
DR P-PSDB; ADR29240.
XX Identifying a compound that modulates the activity of a T1R or T2R taste
PT receptor by assaying the effect of the putative modulatory compound on
PT MAPK activation, CAMP accumulation or adenylyl cyclase activity in the
PT eukaryotic cell.
XX Disclosure; SEQ ID NO 178; 248pp; English.

CC This invention is related to a novel method of identifying a compound
CC that modulates the activity of a T1R or T2R taste receptor. The method
CC comprises providing a eukaryotic cell that expresses a functional T1R or
CC T2R taste receptor and a G protein that couples to it, contacting the
CC eukaryotic cell with a compound and identifying whether the compound
CC modulates the activity of T1R or T2R expressed by the eukaryotic cell
CC based on its effect on MAPK activity, CAMP accumulation or adenylyl
CC cyclase activity. The method is used to identify a compound that blocks
CC bitter taste associated with a particular T2R activator or that blocks or
CC enhances umami taste elicited by a compound that activates the T1R/T1R3
CC (umami) taste receptor or sweet taste elicited by a compound that
CC activates the T1R2/T1R3 (sweet) taste receptor. The method is useful in
CC identifying a compound that modulates the activity of a T1R or T2R taste
CC receptor. The present sequence is that of a gene which encodes a human
CC T2R taste receptor and which is related to the method of the invention.

SQ Sequence 930 BP; 255 A; 177 C; 179 G; 319 T; 0 U; 0 Other;
Query Match 100.0%; Score 930; DB 13; Length 930;
Best Local Similarity 100.0%; Pred. No. 1.2e-247;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATACTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGTACATTTGTATTGGA 60
|||||

DB 1 ATGATACTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGTACATTTGTATTGGA 60
QY 61 AATTTTGTATATGGCTTCATAGCACTGGTAATTCATTTAGTGGTTCAGAGACAAAAG 120
|||||
DB 61 AATTTTGTATATGGCTTCATAGCACTGGTAATTCATTTAGTGGTTCAGAGACAAAAG 120
|||||
QY 121 ATCTCCTTTGTGACCAAATTCCTCACTGCTCTGGGGGTCTCCAGAGTTGGTTGTCTGG 180
121 ATCTCCTTTGTGACCAAATTCCTCACTGCTCTGGGGGTCTCCAGAGTTGGTTGTCTGG 180
|||||
QY 181 GTATTATTATAAAGCTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTAGAAGTA 240
181 GTATTATTATAAAGCTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTAGAAGTA 240
|||||
QY 241 AGAATCTACTGCTTATAATATCTGGGCAGTGAATCAACCAATTTTCAGCAACTGGCTTCTACT 300
241 AGAATCTACTGCTTATAATATCTGGGCAGTGAATCAACCAATTTTCAGCAACTGGCTTCTACT 300
|||||
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCGCAATTTCTCAACTTTATTTTCTTCTAC 360
301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCGCAATTTCTCAACTTTATTTTCTTCTAC 360
|||||
QY 361 TTAAGAGGAGAGTTAAGAGTGTCACTCTGGTGATGTTGTTGGGGCCTTTGCTATTTTGG 420
361 TTAAGAGGAGAGTTAAGAGTGTCACTCTGGTGATGTTGTTGGGGCCTTTGCTATTTTGG 420
|||||
QY 421 GCTTGTCTATCTTTTGTGATAAACAATGAATGAGATTGTGCGGACAAAAGAAATTTGAAGA 480
421 GCTTGTCTATCTTTTGTGATAAACAATGAATGAGATTGTGCGGACAAAAGAAATTTGAAGA 480
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QY 481 AACATGACTTGGAGATCAAAATTGAAGAGTGAATGTAATTTTCAAAATATGACTGTAAACC 540
481 AACATGACTTGGAGATCAAAATTGAAGAGTGAATGTAATTTTCAAAATATGACTGTAAACC 540
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QY 541 ATGTTAGCAAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTATCTGT 600
541 ATGTTAGCAAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTATCTGT 600
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QY 601 TCTTTGTGTAACATCTCAAGAAGATGAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660
601 TCTTTGTGTAACATCTCAAGAAGATGAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660
|||||
QY 661 ACCAAGTCCACATAAAGACTTTTGAAGTGAATCTCTTCTCTTGTATGTGCCATT 720
661 ACCAAGTCCACATAAAGACTTTTGAAGTGAATCTCTTCTCTTGTATGTGCCATT 720
|||||
QY 721 TACTTCTGTCCTAATATGATATCAGTTTGGAGTTTGGAGTCTGGAAAACAAACCTGTC 780
721 TACTTCTGTCCTAATATGATATCAGTTTGGAGTTTGGAGTCTGGAAAACAAACCTGTC 780
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QY 781 TTCATGTTCTGCAAGCTATTAGATTTCAGCTATCTTCAATCCACCCATTTCATCTCTGATT 840
781 TTCATGTTCTGCAAGCTATTAGATTTCAGCTATCTTCAATCCACCCATTTCATCTCTGATT 840
|||||
QY 841 TGGGAAACAGAGAGCTTAAAGCAGACTTTTCTTTCAGTTTTTGGCAAAATGAGGTACTGG 900
841 TGGGAAACAGAGAGCTTAAAGCAGACTTTTCTTTCAGTTTTTGGCAAAATGAGGTACTGG 900
|||||
QY 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930
901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930
|||||
RESULT 6
ID ACC44478 standard; DNA; 1179 BP.
XX ACC44478
AC ACC44478;
XX 25-JUL-2003 (first entry)
XX Gene encoding human GI endocrine cell specific GPCR GT2R-h57.
XX

KW Chemosensor; G-protein coupled receptor; gene; ds; GPCR; receptor;
KW gastrointestinal tract; taste; ion channel; enteroendocrine cell.
XX
OS Homo sapiens.
XX
PN WO2003031604-A1.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032664.
XX
PR 12-OCT-2001; 2001US-0328993P.
XX
PA (REGC) UNIV CALIFORNIA.
PA (PHLE/) PHLEGER C S W.
XX
PI Walsh JH, Rozengurt JE, Wu SV;
XX WPI: 2003-381713/36.
DR P-PSDB; ABR58042.
XX
PT New nucleic acid encoding a chemosensing G-protein coupled receptor,
PT useful for identifying chemical sensing receptors and signaling molecules
PT that allow pharmacological and genetic modulation of taste transduction
PT pathways.
XX
PS Claim; Page 96; 101pp; English.
XX
CC This sequence represents a gene encoding a novel isolated chemosensing G-
CC protein coupled receptor (GPCR) from the gastrointestinal tract. The
CC nucleic acid is useful for identifying or isolating chemical sensing
CC receptors (including taste ion channels) and signaling molecules that
CC would allow pharmacological and genetic modulation of taste transduction
CC pathways. The native STC-1 enteroendocrine cells that naturally express
CC GR2R are useful in identifying modulators of taste receptor-mediated
CC signal transduction. These cells are also used as models for studying
CC taste-mediated signal transduction
XX
SQ Sequence 1179 BP; 314 A; 251 C; 226 G; 388 T; 0 U; 0 Other;
Query Match 100.0%; Score 930; DB 8; Length 1179;
Best Local Similarity 100.0%; Pred. No. 1.3e-247;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATTAACCTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
DB 250 ATGATAAATTTTCTACCCATCAATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 309
QY 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAG 120
DB 310 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAG 369
QY 121 ATCTCTTTTGTGACAAATTTCTACTGCTCTGGGGGCTCCAGAGTTGGTTTGTCTGG 180
DB 370 ATCTCTTTTGTGACAAATTTCTACTGCTCTGGGGGCTCCAGAGTTGGTTTGTCTGG 429
QY 181 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTAATAGTGTAGAGTA 240
DB 430 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTAATAGTGTAGAGTA 489
QY 241 AGAACTACTGCTTATAATATCTGGGAGTGATCAACCAATTTTCAGCAACTGGCTTGTCTACT 300
DB 490 AGAACTACTGCTTATAATATCTGGGAGTGATCAACCAATTTTCAGCAACTGGCTTGTCTACT 549
QY 301 ACCCTCAGCATATTTTATTGTTCAAGATTTGCAATTTCTCAACTTTTATTATTCTTCTAC 360
DB 550 ACCCTCAGCATATTTTATTGTTCAAGATTTGCAATTTCTCAACTTTTATTATTCTTCTAC 609
QY 361 TTAAGAGAGAGATTAAAGAGTGTCTCTGTTGATGTTGTTGGGCTTTGCTATTATTG 420
DB 610 TTAAGAGAGAGATTAAAGAGTGTCTCTGTTGATGTTGTTGGGCTTTGCTATTATTG 669
QY 421 GCTTGTGTCATCTTTTGTGATAAATGATGAGATTGTGCGGACAAAAGAAATTTGAAGGA 480

Db 670 GCTTGTGTCATCTTTTGTGATAAATGATGAGATTGTGCGGACAAAAGAAATTTGAAGGA 729
QY 481 AACATGACTTGGAAAGATCAAAATTTGAAGAGTGCATTTCTTTTCAATATGACTGTAACC 540
DB 730 AACATGACTTGGAAAGATCAAAATTTGAAGAGTGCATTTCTTTTCAATATGACTGTAACC 789
QY 541 ATGGTAGCAAACTTTAGTACCTTCCATCTGACCTCTACTATCTTTTATGCTGTTAATCTGT 600
DB 790 ATGGTAGCAAACTTTAGTACCTTCCATCTGACCTCTACTATCTTTTATGCTGTTAATCTGT 849
QY 601 TCTTTGTGTAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660
DB 850 TCTTTGTGTAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 909
QY 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCT 720
DB 910 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCT 969
QY 721 TACTTCTGTCATAATGATATCAGTTTGGAGTTTGGAGTCTCGGAAACAAACCTGTC 780
DB 970 TACTTCTGTCATAATGATATCAGTTTGGAGTTTGGAGTCTCGGAAACAAACCTGTC 1029
QY 781 TTTATGTTTCTGCAAGCTATTAGATTCAAGTATCTTCAATCCACCCATTTCACTCTGATT 840
DB 1030 TTTATGTTTCTGCAAGCTATTAGATTCAAGTATCTTCAATCCACCCATTTCACTCTGATT 1089
QY 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGGTACTGG 900
DB 1090 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGGTACTGG 1149
QY 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930
DB 1150 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 1179
RESULT 7
ADC87038
ID ADC87038 standard; DNA; 1330 BP.
XX AC ADC87038;
XX AC ADC87038;
DT 01-JAN-2004 (first entry)
XX Human GPCR gene SEQ ID NO:1491.
DE ds; gene; human; GPCR;
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
KW Homo sapiens.
OS
XX EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
DR WPI: 2003-315783/31.
DR P-PSDB; ADC87039.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 1491; 28pp; English.
XX

CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC95548-ADC87616 encode GPCR's of the
CC invention.

XX SQ Sequence 1330 BP; 369 A; 258 C; 253 G; 450 T; 0 U; 0 Other;
Query Match 100.0%; Score 930; DB 10; Length 1330;
Best Local Similarity 100.0%; Pred. No. 1.4e-247;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTTCCAGTCTGAGTGGTTACATTTGTTATTGGA 60
DB 201 ATGATAACTTTTCTACCCATCATTTTTTCCAGTCTGAGTGGTTACATTTGTTATTGGA 260
QY 61 AATTTTGTAAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAAG 120
DB 261 AATTTTGTAAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAAG 320
QY 121 ATCTCTTTTGTGACCAATCTCACTGCTGCGGCTCCAGAGTTGGTTGCTCTGG 180
DB 321 ATCTCTTTTGTGACCAATCTCACTGCTGCGGCTCCAGAGTTGGTTGCTCTGG 380
QY 181 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
DB 381 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 440
QY 241 AGAAGTCTGCTTAATAATATCGGCGAGTATCAACCAATTCAGCAACTGGCTGCTACT 300
DB 441 AGAAGTCTGCTTAATAATATCGGCGAGTATCAACCAATTCAGCAACTGGCTGCTACT 500
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCAACTTTATTTCTTCAC 360
DB 501 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAATTTCTCAACTTTATTTCTTCAC 560
QY 361 TTAAGAGGAGATTAAAGAGTGTCAATCTGAGTGTGTTGGGCGCTTTGCTATTTTG 420
DB 561 TTAAGAGGAGATTAAAGAGTGTCAATCTGAGTGTGTTGGGCGCTTTGCTATTTTG 620
QY 421 GCTTGTCATCTTTTGTGATAAACATGAATGAGATTGTCGGAACAAAGAAATTTGAAGGA 480
DB 621 GCTTGTCATCTTTTGTGATAAACATGAATGAGATTGTCGGAACAAAGAAATTTGAAGGA 680
QY 481 AACATGACTTGAAGATCAAAATGAAGAGTGCATGTACTTTTCAAAATGACTGTAAAC 540
DB 681 AACATGACTTGAAGATCAAAATGAAGAGTGCATGTACTTTTCAAAATGACTGTAAAC 740
QY 541 ATGCTAGCAAACTTAGTACCCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGT 600
DB 741 ATGCTAGCAAACTTAGTACCCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGT 800
QY 601 TCTTTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCCAAGC 660
DB 801 TCTTTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCCAAGC 860
QY 661 ACCAAGTCCACATAAAGCTTGCATACTGTGATCTCTTCTCTTGTATGTCCTATT 720
DB 861 ACCAAGTCCACATAAAGCTTGCATACTGTGATCTCTTCTCTTGTATGTCCTATT 920
QY 721 TACTTTCTGTCCATAATGATATCAGTTTGGAGTGTGGAAGTCTGGAAAAACAAACCTGTC 780
DB 921 TACTTTCTGTCCATAATGATATCAGTTTGGAGTGTGGAAGTCTGGAAAAACAAACCTGTC 980
QY 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCATCTGATT 840
DB 981 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCATCTGATT 1040
QY 841 TGGGGAACAGAGCTAAAGCAGCTTTTCTTTTCAGTTTCTTTGGCAATGAGTACTGG 900

Db 1041 TGGGGAACAGAGCTAAAGCAGACTTTTCTTTTCAGTTTCTTTGGCAATGAGGTAAGTGG 1100
QY 901 GTGAAAGGAGAGAGACTTCTATCTCCATAG 930
DB 1101 GTGAAAGGAGAGAGACTTCTATCTCCATAG 1130
RESULT 8
ADM74419
ID ADM74419 standard; DNA; 930 BP.
XX AC ADM74419;
XX DT 07-APR-2005 (first entry)
XX Human bitter taste receptor gene T2R43 with a coding SNP Seq 31.
XX SNP detection; SNP; single nucleotide polymorphism; screening;
XX DNA microarray; flavor enhancer; ds; gene.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..930
FT /*tag= a /product= "T2R protein"
FT 104
FT variation /*tag= b /standard_name= "Single nucleotide polymorphism"
FT 270
FT variation /*tag= c /standard_name= "Single nucleotide polymorphism"
FT 460
FT variation /*tag= d /standard_name= "Single nucleotide polymorphism"
FT 510
FT variation /*tag= e /standard_name= "Single nucleotide polymorphism"
FT 599
FT variation /*tag= f /standard_name= "Single nucleotide polymorphism"
FT 635
FT variation /*tag= g /standard_name= "Single nucleotide polymorphism"
FT 663
FT variation /*tag= h /standard_name= "Single nucleotide polymorphism"
FT 882
FT variation /*tag= i /standard_name= "Single nucleotide polymorphism"
FT 883
FT variation /*tag= j /standard_name= "Single nucleotide polymorphism"
FT 889
FT variation /*tag= k /standard_name= "Single nucleotide polymorphism"
XX WO2005007891-A2.
XX 27-JAN-2005.
XX 18-JUN-2004; 2004WO-US019489.
XX 19-JUN-2003; 2003US-0480035P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Drayna D, Kim U;
XX WPI; 2005-152091/16.
XX P-PSDB; ADM74420.
XX New isolated bitter taste receptor (T2R) variant-specific nucleic acid

PT molecule comprises at least 10 contiguous nucleotides, useful for
PT defining large groups of populations who perceive bitter tastes
PT differently.

Claim 1; SEQ ID NO 31; 567pp; English.

This invention relates to novel human bitter taste receptor (T2R) variant -specific nucleic acid molecules, each spanning at least one SNP identified in the specification. Specifically, it refers to the T2R allele nucleic acid molecules and the encoded proteins thereof. The present invention describes a method of screening compounds useful for modulating bitter taste and using a specific binding agent that is capable of discriminating between two or more polypeptides. Accordingly, it provides a method of determining the T2R genotype of a subject using at least one oligonucleotide from each T2R haplotype/allele on a microarray to identify T2R single nucleotide polymorphisms. As such, the isolated T2R variant-specific nucleic acid molecules are useful in the development of flavorings and flavor enhancers as it can be used to define large groups of populations who perceive bitter tastes differently. It is also used to identify compounds that interact differently with different variants of a taste receptor. This polynucleotide sequence is a bitter taste receptor T2R gene of the invention.

Sequence 930 BP; 253 A; 175 C; 176 G; 316 T; 0 U; 10 Other;

Query Match 99.4%; Score 924; DB 14; Length 930;
Best Local Similarity 98.9%; Pred. No. 5.7e-246;
Matches 918: Conservative 10; Mismatches 0; Indels

| | | | |
|----|-----|--|-----|
| Qy | 1 | ATGATAACCTTTTCTACCCCAATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA | 60 |
| Db | 1 | ATGATAACCTTTTCTACCCCAATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA | 60 |
| Qy | 61 | AAATTTTGCTAAATGGCTTCATAGCACTGGTAAATCCATTTGAGTGGTTCAAGAGACAAAAAG | 120 |
| Db | 61 | AAATTTTGCTAAATGGCTTCATAGCACTGGTAAATCCATTTGAGTGGTTCAAGAGACAAAAAG | 120 |
| Qy | 121 | ATCTCCTTTTGGCTGACCAAAATTTCTCACTGCTCTGGGGGTCTCCAGAGTTGGTTTGGCTCTGG | 180 |
| Db | 121 | ATCTCCTTTTGGCTGACCAAAATTTCTCACTGCTCTGGGGGTCTCCAGAGTTGGTTTGGCTCTGG | 180 |
| Qy | 181 | GTATATTATTAAACTGGSTATTCAACTGTGTGTAATCCAGCTTTTAATAGTGTAGAAGTA | 240 |
| Db | 181 | GTATATTATTAAACTGGSTATTCAACTGTGTGTAATCCAGCTTTTAATAGTGTAGAAGTA | 240 |
| Qy | 241 | AGAACTACTGCTTTATAATATCTGGGCAGTGTCAACCAATTTTCAGCAACTCGCTTGGCTACT | 300 |
| Db | 241 | AGAACTACTGCTTTATAATATCTGGGCAGTGTCAACCAATTTTCAGCAACTCGCTTGGCTACT | 300 |
| Qy | 301 | ACCTCTCAGCATATTTTATATTTGTCTCAAGATATGCCAAATTTCTCCAACTTTATTTTCTTCAC | 360 |
| Db | 301 | ACCTCTCAGCATATTTTATATTTGTCTCAAGATATGCCAAATTTCTCCAACTTTATTTTCTTCAC | 360 |
| Qy | 361 | TTAAAGAGGAGAGTTTAAAGAGTGTCAATCTGTGTGATGTTTGTGGGGCCCTTTTGCTATTTTGTG | 420 |
| Db | 361 | TTAAAGAGGAGAGTTTAAAGAGTGTCAATCTGTGTGATGTTTGTGGGGCCCTTTTGCTATTTTGTG | 420 |
| Qy | 421 | GCTTTGTTCATCTTTTGTGTGATAAACAATGAGATATGTGCGGACAAAGAAGATTTGAAGGA | 480 |
| Db | 421 | GCTTTGTTCATCTTTTGTGTGATAAACAATGAGATATGTGCGGACAAAGAAGATTTGAAGGA | 480 |
| Qy | 481 | AACATGACTTTGGAAGATCAAAATTTGAAGAGTGCAAATGTACTTTTCAAATATGACTGTAAACC | 540 |
| Db | 481 | AACATGACTTTGGAAGATCAAAATTTGAAGAGTGCAAATGTACTTTTCAAATATGACTGTAAACC | 540 |
| Qy | 541 | ATGGTAGCAAAACTTAGTAGCCCTTCACTCTGACCCCTAATACTTTTATGCTGTTAAATCTGT | 600 |
| Db | 541 | ATGGTAGCAAAACTTAGTAGCCCTTCACTCTGACCCCTAATACTTTTATGCTGTTAAATCTKT | 600 |
| Qy | 601 | TCCTTTGTGTAAACATCTCAAGAAGATGCAGAGCTCCATGGTAAAGGATCTCAAGATCCACAGC | 660 |
| Db | 601 | TCCTTTGTGTAAACATCTCAAGAAGATGCAGCTCCCTGTGTAAAGCATCTCAGATCCACAGC | 660 |

CC isolating (M1) a compound that binds to (V) encoded by (I); (10)
CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a
CC foodstuff including human and animal foodstuff, any precursor material or
CC additive employed in the production of foodstuff comprising (VIII); and
CC (12) a nutraceutical/pharmaceutical composition comprising (VIII) and an
CC active agent and optionally a carrier. (III) is useful for producing a
CC polypeptide encoded by (I), which involves culturing (III) and recovering
CC the polypeptide encoded by (I). (II) is useful for producing cells
CC capable of expressing at least one of the bitter taste receptor
CC polypeptide, which involves genetically cells in vitro with (II), where
CC the bitter taste receptor polypeptide(s) is/are encoded by (I). (M1) or
CC (M2) can be used for producing food or any precursor material or additive
CC employed in the production of foodstuffs. (M1) or (M2) can also be used
CC for producing nutraceutical or pharmaceutical compositions. (I), (II),
CC (VI) or (VIII) can be used for manufacturing a medicament for the
CC treatment of an abnormally increased or decreased sensitivity towards a
CC bitter substance. The identified agonist/inhibitor efficiently suppresses
CC or eliminates bitter tasting components of food and effectively useful in
CC food industries.

XX
SQ Sequence 927 BP; 253 A; 177 C; 179 G; 318 T; 0 U; 0 Other;

Query Match 99.2%; Score 922.2; DB 13; Length 927;
Best Local Similarity 99.7%; Pred. No. 1.8e-245;
Matches 924; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTTCCAGTCTGTGTAGTGTACATTTGTTATTGGA 60
Db 1 ATGATAACTTTTCTACCCATCATTTTTTCCAGTCTGTGTAGTGTACATTTGTTATTGGA 60
QY 61 AATTTTGCTAATGGCTTCATAGCAGCTGTTAAATCCATTGAGTGGTTCAGAGACAAAAG 120
Db 61 AATTTTGCTAATGGCTTCATAGCAGCTGTTAAATCCATTGAGTGGTTCAGAGACAAAAG 120
QY 121 ATCTCTTTGCTGACCAAAATCTCACTGCTCTGCGGCTCTCCAGAGTGGTTCCTGCTG 180
Db 121 ATCTCTTTGCTGACCAAAATCTCACTGCTCTGCGGCTCTCCAGAGTGGTTCCTGCTG 180
QY 181 GTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAGTA 240
Db 181 GTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAGTA 240
QY 241 AGAAGTACTGCTTATTAATATCTGGGAGTATCAACCATTTGCAAGCTGGCTGTACT 300
Db 241 AGAAGTACTGCTTATTAATATCTGGGAGTATCAACCATTTGCAAGCTGGCTGTACT 300
QY 301 ACCCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCCAACTTTTATTTTCTTAC 360
Db 301 ACCCTCAGCATATTTTATTGCTCAAGATTGCCAATTTCTCCAACTTTTATTTTCTTAC 360
QY 361 TTAAGAGAGAGATTAAAGAGTGTCAATCTGTTGATGTTGTTGGGCTTTGCTATTTTGG 420
Db 361 TTAAGAGAGAGATTAAAGAGTGTCAATCTGTTGATGTTGTTGGGCTTTGCTATTTTGG 420
QY 421 GCTTGTCACTTTTGTGATAAATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 GCTTGTCACTTTTGTGATAAATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 AACATCACTTTGGAAGATCAAAATGGAAGTGCATCTTTTCAATATGATGATGATGATGAT 540
Db 481 AACATCACTTTGGAAGATCAAAATGGAAGTGCATCTTTTCAATATGATGATGATGATGAT 540
QY 541 ATGGTAGCAAACTTAGTACCTTTCACTCTGACCTACTATCTTTTATGCTGTTAACTCTG 600
Db 541 ATGGTAGCAAACTTAGTACCTTTCACTCTGACCTACTATCTTTTATGCTGTTAACTCTG 600
QY 601 TCTTTGTGTAACATCTCAAGAGATGCGAGCTCCGTTGGTAAAGGATCTCAAGATCCGAGC 660
Db 601 TCTTTGTGTAACATCTCAAGAGATGCGAGCTCCGTTGGTAAAGGATCTCAAGATCCGAGC 660
QY 661 ACCAAGGTCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 661 ACCAAGGTCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 720

QY 721 TACTTTCTCTCCATAATGATATCAGTTTGGAGTCTTGGAGTCTGGAACCAAACTGTC 780
Db 721 TACTTTCTCTCCATAATGATATCAGTTTGGAGTCTTGGAGTCTGGAACCAAACTGTC 780
QY 781 TTCAATGTTCTGCAAGCTATTAGATTACGATATCTTCAATCCACCATTTCATCTGATT 840
Db 781 TTCAATGTTCTGCAAGCTATTAGATTACGATATCTTCAATCCACCATTTCATCTGATT 840
QY 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTCTTTTGGCAAAATGAGGTACTGG 900
Db 841 TGGGGAACCAAGAGCTAAAGCAGACTTTTCTTCAAGTCTTTTGGCAAAATGAGGTACTGG 900
QY 901 GTCAAGAGGAGAGACTTTTCATCTCCA 927
Db 901 GTCAAGAGGAGAGACTTTTCATCTCCA 927
RESULT 10
ADW74575
ID ADW74575 standard; DNA; 930 BP.
XX
AC ADW74575;
XX
DT 07-APR-2005 (first entry)
XX
DE Human bitter taste receptor haplotype gene T2R44 Seq 187.
XX
KW SNP detection; SNP; single nucleotide polymorphism; screening;
KW DNA microarray; flavor enhancer; ds; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..930
FT /*tag= a /product= "T2R protein"
FT replace(103,c)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT replace(484,t)
FT /*tag= c
FT /standard_name= "Single nucleotide polymorphism"
FT replace(599,a)
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT replace(649,g)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT replace(656,t)
FT /*tag= f
FT /standard_name= "Single nucleotide polymorphism"
FT replace(680,c)
FT /*tag= g
FT /standard_name= "Single nucleotide polymorphism"
FT replace(718,g)
FT /*tag= h
FT /standard_name= "Single nucleotide polymorphism"
FT replace(827,g)
FT /*tag= i
FT /standard_name= "Single nucleotide polymorphism"
FT replace(843,t)
FT /*tag= j
FT /standard_name= "Single nucleotide polymorphism"
XX
PN WO2005007891-A2.
XX
PD 27-JAN-2005.
XX
PF 18-JUN-2004; 2004WO-US019489.
XX
PR 19-JUN-2003; 2003US-0480035P.
XX

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Drayna D, Kim U;

WPI; 2005-152091/16.

P-PSDB; ADW74576.

New isolated bitter taste receptor (T2R) variant-specific nucleic acid molecule comprises at least 10 contiguous nucleotides, useful for defining large groups of populations who perceive bitter tastes differently.

Claim 9; SEQ ID NO 187; 567pp; English.

This invention relates to novel human bitter taste receptor (T2R) variant -specific nucleic acid molecules, each spanning at least one SNP identified in the specification. Specifically, it refers to the T2R allele nucleic acid molecules and the encoded proteins thereof. The present invention describes a method of screening compounds useful for modulating bitter taste and using a specific binding agent that is capable of discriminating between two or more polypeptides. Accordingly, it provides a method of determining the T2R genotype of a subject using at least one oligonucleotide from each T2R haplotype/allele on a microarray to identify T2R single nucleotide polymorphisms. As such, the isolated T2R variant-specific nucleic acid molecules are useful in the development of flavorings and flavor enhancers as it can be used to define large groups of populations who perceive bitter tastes differently. It is also used to identify compounds that interact differently with different variants of a taste receptor. This polynucleotide sequence is a bitter taste receptor T2R haplotype gene of the invention.

Sequence 930 BP; 246 A; 177 C; 192 G; 315 T; 0 U; 0 Other;

Query Match 91.7%; Score 852.8; DB 14; Length 930;

Best Local Similarity 94.9%; Pred. No. 3.4e-226;

Matches 881; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ATGATTAACCTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
XX |||||
PI |||||
XX 1 ATGACAACCTTTTATACCCATCATTTTTTCCAGTCTGGTAGTGGTTCTATTGTTATTGGA 60
QY 61 AATTTTGCTAATGGCTTCATAGCAGCTGTAATTCATTGAGTGGTTCAAGAGACAAAAG 120
DB |||||
XX 61 AATTTTGCTAATGGCTTCATAGCAGTGGTAATTCATTGAGTGGTCAAGAGACAAAAG 120
QY 121 ATCTCTTTGCTGACCAAAATTCCTACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180
DB |||||
XX 121 ATCTCTTTGCTGACCAAAATTCCTACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180
QY 181 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAAGTA 240
DB |||||
XX 181 GTATTATTATTAAATGGTATTCAACTGTGTTTAATCCAGCTTTTATAGTGTAGAAGTA 240
QY 241 AGAAGTACTGCTTATATATCTGGGAGTGATCAACATTTTCAGCAACTGGCTTGTCTACT 300
DB |||||
XX 241 AGAAGTACTGCTTATATATCTGGGAGTGATCAACGAGCAATTCAGCAACTGGCTTGTCTACT 300
QY 301 ACCCTCAGCATATTTTATTGCTCAAGATGCGCAATTTCTCAACTTTATTTTCTTCTAC 360
DB |||||
XX 301 AGCCTCAGCATATTTTATTGCTCAAGATGCGCAATTTCTCAACCTTATTTTCTTCTAC 360
QY 361 TTAAGAGAGAGATTAAAGAGTGTCTGTTGATGTTGTTGGGCTTGTCTATTTTTG 420
DB |||||
XX 361 TTAAGAGAGAGATTAAAGAGTGTCTGTTGATGTTGTTGGGCTTGTCTATTTTTG 420
QY 421 GCTTGTCTATCTTTTGTGATAAATGAGATTGTGCGGACAAAAGAAATTTGAAGA 480
DB |||||
XX 421 GCTTGTCTATCTTTTGTGATAAATGAGATTGTGCGGACAAAAGAAATTTGAAGA 480
QY 481 AACATGACTTGGAGATCAAAATGGAAGTGCATGTACTTTTCAAAATATGACTGTAAAC 540
DB |||||
XX 481 AACATGACTTGGAGATCAAAATGGAAGTGCATGTACTTTTCAAAATATGACTGTAAAC 540

XX The invention relates to a mammalian taste cell-specific G protein-
CC coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste
CC sensation. The T2R polypeptides and their associated polynucleotides are
CC useful for screening one or more compounds for the presence of taste
CC detectable by a mammal. Modulators of T2R polypeptides (modulators of
CC taste transduction) are useful for pharmacological and genetic
CC modulations of taste signalling pathways. These modulatory compounds are
CC then used in food and pharmaceutical industries to customise taste, e.g.,
CC to decrease or mask the bitter taste of foods or drugs. This sequence
CC represents cDNA encoding the human T2R64 (hT2R64) polypeptide
XX
SQ Sequence 930 BP; 244 A; 179 C; 193 G; 314 T; 0 U; 0 Other;

Query Match 91.6%; Score 851.6; DB 6; Length 930;
Best Local Similarity 94.7%; Pred. No. 7.2e-226;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTCACGTCGTGGTAGTGGTTACATTGTTATTGGA 60
DB 1 ATGACAACCTTTATACCCATCATTTTTCACGTCGTGGTAGTGGTTCTATTGTTATTGGA 60
QY 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120
DB 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120
QY 121 ATCTCTTTGTGACAAATTCATCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
DB 121 ATCTCTTTGTGACAGATTCATCTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
QY 181 GTATTATTATTAACCTGTTATTCACCTGTTGTAATCCAGCTTTTAATAGTGTAGAATA 240
DB 181 GTATTATTATTAACCTGTTATTCACCTGTTGTAATCCAGCTTTTAATAGTGTAGAATA 240
QY 241 AGAATCTGCTTATAATATCTGGCAGTGATCAACCACTTCAGCAACTGGCTCTACT 300
DB 241 AGAATCTGCTTATAATATCTGGCAGTGATCAACCACTTCAGCAACTGGCTCTACT 300
QY 301 ACCCTCAGCATATTTATTTGCTCAAGATGCAATTTCTCAACTTTATTTTCTTCAC 360
DB 301 AGCCTCAGCATATTTATTTGCTCAAGATGCAATTTCTCAACTTTATTTTCTTCAC 360
QY 361 TTAAGAGAGAGTTAAGAGTGTCACTCTGGTAGTGGTTGGGCGCTTGTCTATTTTG 420
DB 361 TTAAGAGAGAGTTAAGAGTGTCACTCTGGTAGTGGTTGGGCGCTTGTCTATTTTG 420
QY 421 GCTTGTCTATCTTTTGTGATAAATGATGATGATGTCGCGACAAAGAAATTTGAAGA 480
DB 421 GCTTGTCTATCTTTTGTGATAAATGATGATGATGTCGCGACAAAGAAATTTGAAGA 480
QY 481 AACATGACTTGAAGATCAAAATTTGAAGAGTGAATGTACTTTTCAAAATGACTGTAAAC 540
DB 481 AACTTGTACTTGAAGATCAAAATTTGAAGAGTGAATGTACTTTTCAAAATGACTGTAAAC 540
QY 541 ATGTAGCAAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTTAATCTGT 600
DB 541 ACCTTAGGAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTTAATCTGT 600
QY 601 TCTTTGTGAACATCTCAAGAGATGTCAGCTCCATGTTAAGGATCTCAAGATCCGAGC 660
DB 601 TCTTGTGTAACATCTCAAGAGATGTCAGCTCCATGTTAAGGATCTCAAGATCCGAGC 660
QY 661 ACCAAGTCCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTCTTTATGTGCCATT 720
DB 661 ACCAAGTCCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTCTTTATGTGCCATT 720
QY 721 TACTTTCTGTCATTAATGATATCATGTTGGAGTTTGGAAAGTCTGGAAAAACAACCTGTC 780
DB 721 TACTTTCTGTCATTAATGATATCATGTTGGAGTTTGGAGTCTGGAAAAACAACCTGTC 780
QY 781 TTCAATGTTCTCAAGAGCTATTAGATTCAGCTATCTCTCAATCCACCCATTCCTGATT 840
DB 781 TTCAATGTTCTCAAGAGCTATTAGATTCAGCTATCTCTCAATCCACCCATTCCTGATT 840

QY 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGTACTGG 900
DB 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCGCAAGTGAGTACTGG 900
QY 901 GTGAAGGAGAGAGAGACTTCATCTCCATAG 930
DB 901 GTGAAGGAGAGAGAGACTTCATCTCCATAG 930

RESULT 12

ABZ43215
ID ABZ43215 standard; DNA; 930 BP.

XX AC ABZ43215;

XX DT 06-MAR-2003 (first entry)

XX Human GPCR polynucleotide SEQ ID NO 691.

DE Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; gene; ds.

XX OS Homo sapiens.

XX PN WO200216548-A2.

XX PD 28-FEB-2002.

XX PF 30-JUL-2001; 2001WO-1B001446.

XX PR 04-AUG-2000; 2000JP-00237818.

XX PR 13-FEB-2001; 2001JP-00034434.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Haga T, Takeda S, Mitaku S;

XX WPI; 2002-304118/34.

XX P-PSDB; ABP95941.

PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.

PS Claim 9; SEQ ID NO 691; 97pp + Sequence Listing; Japanese.

CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 930 BP; 244 A; 179 C; 193 G; 314 T; 0 U; 0 Other;

Query Match 91.6%; Score 851.6; DB 6; Length 930;

Best Local Similarity 94.7%; Pred. No. 7.2e-226;

Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTTCACGTCGTGGTAGTGGTTACATTGTTATTGGA 60

DB 1 ATGACAACCTTTATACCCATCATTTTTCACGTCGTGGTAGTGGTTCTATTGTTATTGGA 60

QY 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120

DB 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120

QY 121 ATCTCCTTTGCTGACCAAAATCTCACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||
QY 121 ATCTCCTTTGCTGACCAAAATCTCACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||
QY 181 GTATTATTATAAATCTGATTTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
QY 181 GTATTATTATAAATCTGATTTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGAATCAACCAATTCAGCAACTGGCTGCTACT 300
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGAATCAACCAATTCAGCAACTGGCTGCTACT 300
Db |||||
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGAATTTCTCAACTTTATTTTCTTCCAC 360
Db |||||
QY 301 AGCCTCAGCATATTTTATTTGCTCAAGATTCGAATTTCTCAACTTTATTTTCTTCCAC 360
Db |||||
QY 361 TTAAGAGGAGATTAAGAGTGTCAATCTGTGTGATGCTGTGGGGCTTTACTATTTTG 420
Db |||||
QY 361 TTAAGAGGAGATTAAGAGTGTCAATCTGTGTGATGCTGTGGGGCTTTACTATTTTG 420
Db |||||
QY 421 GCTTGTCAATCTTTTGTGATTAACATGAATGAGATTTGGGAGCAAAAAGAAATTTGAAGGA 480
Db |||||
QY 421 GCTTGTCAATCTTTTGTGATTAACATGAATGAGATTTGGGAGCAAAAAGAAATTTGAAGGA 480
Db |||||
QY 481 AACATGACTTGGAGATCAAAATTTGAAGTGCATTTTCAAAATGACTGTAAACC 540
Db |||||
QY 481 AACATGACTTGGAGATCAAAATTTGAAGTGCATTTTCAAAATGACTGTAAACC 540
Db |||||
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATCTGTAAATCTGT 600
Db |||||
QY 541 ACGCTAGGAACCTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTGTCTGTAAATCTGT 600
Db |||||
QY 601 TCTTTGTGAACATCTCAAGAAGATGAGCTCCATGATGAAGATCTCAAGATCCCAAG 660
Db |||||
QY 601 TCTTGTGTGAACATCTCAAGAAGATGAGCTCCATGATGAAGATCTCAAGATCCCAAG 660
Db |||||
QY 661 ACCAGGTCCCATAAAGCTTTGCAAACTGTGATCTCTTCTCTCTGTTATGTCCTATT 720
Db |||||
QY 661 ACCAAGGTCCCATAAAGCTTTGCAAACTGTGATCTTTTCTCTCTGTTATGTCCTATT 720
Db |||||
QY 721 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAAAGTCTGGAAAACAAACCTGTC 780
Db |||||
QY 721 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAGTCTGGAAAACAAACCTGTC 780
Db |||||
QY 781 TTCATGTTCTGCAAAAGCTATTAGATTCAGCTATCCCTTCAATCCCAATTCATCTGATT 840
Db |||||
QY 781 TTCATGTTCTGCAAAAGCTATTAGATTCAGCTATCCCTTCAATCCCAATTCATCTGATT 840
Db |||||
QY 841 TGGGGAACAAGAGCTAAGCAGACTTTTCTTTCAGTTTGTGGCAATGAGGTACTGG 900
Db |||||
QY 841 TGGGGAACAAGAGCTAAGCAGACTTTTCTTTCAGTTTGTGGCAATGAGGTACTGG 900
Db |||||
QY 901 GTGAAGGAGAGAGACTTTCATCTCCATAG 930
Db |||||
QY 901 GTGAAGGAGAGAGACTTTCATCTCCATAG 930
Db |||||

RESULT 13

ACC44476
ID ACC44476 standard; DNA; 930 BP.
XX
XX ACC44476;
AC
XX
XX 25-JUL-2003 (first entry)
XX
XX Gene encoding human GI endocrine cell specific GPCR GT2R-h55.
XX
XX Chemosensor; G-protein coupled receptor; gene; ds; GPCR; receptor;
KW gastrointestinal tract; taste; ion channel; enteroendocrine cell.
XX
XX Homo sapiens.
OS
XX

PN WO2003031604-A1.
XX 17-APR-2003.
PD
XX 11-OCT-2002; 2002WO-US032664.
PF
XX 12-OCT-2001; 2001US-0328993P.
PR
XX (REGC) UNIV CALIFORNIA.
PA (PHLE/) PHLEGER C S W.
PI Walsh JH, Rozengurt JE, Wu SV;
XX WPI; 2003-381713/36.
DR P-PSDB; ABR58040.
XX
PT New nucleic acid encoding a chemosensing G-protein coupled receptor,
PT useful for identifying chemical sensing receptors and signaling molecules
PT that allow pharmacological and genetic modulation of taste transduction
PT pathways.
XX
PS Claim; Page 93; 101pp; English.
XX
CC This sequence represents a gene encoding a novel isolated chemosensing G-
CC protein coupled receptor (GPCR) from the gastrointestinal tract. The
CC nucleic acid is useful for identifying or isolating chemical sensing
CC receptors (including taste ion channels) and signaling molecules that
CC would allow pharmacological and genetic modulation of taste transduction
CC pathways. The native STC-1 enteroendocrine cells that naturally express
CC GT2R are useful in identifying modulators of taste receptor-mediated
CC signal transduction. These cells are also used as models for studying
CC taste-mediated signal transduction
XX

Sequence 930 BP; 244 A; 179 C; 193 G; 314 T; 0 U; 0 Other;
Query Match 91.6%; Score 851.6; DB 8; Length 930;
Best Local Similarity 94.7%; Pred. No. 7.2e-226;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1 ATGATAACTTTTACCCATCATTTTTCAGTCTGGTAGTGGTTTACATTTGTTATTGGA 60
Db |||||
QY 1 ATGCAAACTTTTATACCCATCATTTTTCAGTCTGGTAGTGGTTTATTTGTTATTGGA 60
Db |||||
QY 61 AATTTTGTCTAATGCTTCATAGCACTGTAATTCATTTCCATTTGAGTGTCCAGAGACAAAG 120
Db |||||
QY 61 AATTTTGTCTAATGCTTCATAGCACTGTAATTCATTTCCATTTGAGCGGTCAAGAGACAAAG 120
Db |||||
QY 121 ATCTCCTTTGCTGACCAAAATCTCACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||
QY 121 ATCTCCTTTGCTGACCAAAATCTCACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||
QY 181 GTATTATTATAAATCTGATTTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
QY 181 GTATTATTATAAATCTGATTTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGAATCAACCAATTCAGCAACTGGCTGCTACT 300
Db |||||
QY 241 AGAATCTGCTTATAATATCTGGGAGTGAATCAACCAATTCAGCAACTGGCTGCTACT 300
Db |||||
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGAATTTCTCAACTTTATTTTCTTCCAC 360
Db |||||
QY 301 AGCCTCAGCATATTTTATTTGCTCAAGATTCGAATTTCTCAACTTTATTTTCTTCCAC 360
Db |||||
QY 361 TTAAGAGGAGATTAAGAGTGTCAATCTGTGTGATGCTGTGGGGCTTTACTATTTTG 420
Db |||||
QY 361 TTAAGAGGAGATTAAGAGTGTCAATCTGTGTGATGCTGTGGGGCTTTACTATTTTG 420
Db |||||
QY 421 GCTTGTCAATCTTTTGTGATTAACATGAATGAGATTTGGGAGCAAAAAGAAATTTGAAGGA 480
Db |||||
QY 421 GCTTGTCAATCTTTTGTGATTAACATGAATGAGATTTGGGAGCAAAAAGAAATTTGAAGGA 480
Db |||||
QY 481 AACATGACTTGGAGATCAAAATTTGAAGTGCATTTTCAAAATGACTGTAAACC 540
Db |||||

Db 481 AACTTGACTTGAAGATCAAAATGAGGAGTGAGTGACCTTTTCAGATGCGACTGAACC 540
Qy 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTAACTCTGT 600
Db 541 ACGCTAGGAAACTTAGTGCCCTTCACTCTGACCCCTGCTATGTTTTTGTGTTAATCTGT 600
Qy 601 TCTTTGTGTAAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCGAGC 660
Db 601 TCTCTGTGTAAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCGAGC 660
Qy 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTGTTTATGTCCTATT 720
Db 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTGTTTATGTCCTATT 720
Qy 721 TACTTTCTGTCCATATGATATGATTCAGTTGGAGTTTGGAGTCTCGAAACAAACCTGTC 780
Db 721 TACTTTCTGTCCATATGATATGATTCAGTTGGAGTTTGGAGTCTCGAAACAAACCTGTC 780
Qy 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCACTCTGATT 840
Db 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCACTCTGATT 840
Qy 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGGTACTGG 900
Db 841 TGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGCAAAATGAGGTACTGG 900
Qy 901 GTGAAGGAGAGAGACTTCATCTCCATAG 930
Db 901 GTGAAGGAGAGAGACTTCATCTCCATAG 930

RESULT 14
ID ADR29243
ADR29243 standard; DNA; 930 BP.
XX
AC ADR29243;
XX
DT 04-NOV-2004 (first entry)
XX
DE Taste receptor modulation-related human T2R64 gene sequence SeqID182.
XX
KW T1R; T2R; taste receptor; G protein; modulatory compound; MAPK activity;
KW CAMP accumulation; adenylyl cyclase; bitter; taste; umami; sweet; T2R64;
XX gene; ds; human.
XX
XX Homo sapiens.
XX
XX WO2004069191-A2.
XX
PD 19-AUG-2004.
XX
XX 03-FEB-2004; 2004WO-US002987.
XX
XX 03-FEB-2003; 2003US-0444172P.
XX
XX 26-MAR-2003; 2003US-0457318P.
XX
XX (SENO-) SENOMYX INC.
XX
XX Servant G, Ozeck M, Brust P, Xu H;
XX
XX WPI; 2004-604341/58.
XX
XX P-ESDB; ADR29244.
XX
XX Identifying a compound that modulates the activity of a T1R or T2R taste
XX receptor by assaying the effect of the putative modulatory compound on
XX MAPK activation, CAMP accumulation or adenylyl cyclase activity in the
XX eukaryotic cell.
XX
XX Disclosure; SEQ ID NO 182; 248pp; English.
XX
XX This invention is related to a novel method of identifying a compound
XX that modulates the activity of a T1R or T2R taste receptor. The method
XX comprises providing a eukaryotic cell that expresses a functional T1R or

CC T2R taste receptor and a G protein that couples to it, contacting the
CC eukaryotic cell with a compound and identifying whether the compound
CC modulates the activity of T1R or T2R expressed by the eukaryotic cell
CC based on its effect on MAPK activity, CAMP accumulation or adenylyl
CC cyclase activity. The method is used to identify a compound that blocks or
CC bitter taste associated with a particular T2R activator or that blocks or
CC enhances umami taste elicited by a compound that activates the T1R1/T1R3
CC (umami) taste receptor or sweet taste elicited by a compound that
CC activates the T1R2/T1R3 (sweet) taste receptor. The method is useful in
CC identifying a compound that modulates the activity of a T1R or T2R taste
CC receptor. The present sequence is that of a gene which encodes a human
CC T2R taste receptor and which is related to the method of the invention.
XX
SQ Sequence 930 BP; 244 A; 179 C; 193 G; 314 T; 0 U; 0 Other;
Query Match 91.6%; Score 851.6; DB 13; Length 930;
Best Local Similarity 94.7%; Pred. No. 7.2e-226;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Qy 1 ATGATAAATCTTTTACCCATCATTTTTTCCAGTCTGGTAGTGGTTTACATTTGTTATTGGA 60
Db 1 ATGATAAATCTTTTACCCATCATTTTTTCCAGTCTGGTAGTGGTTTACATTTGTTATTGGA 60
Qy 61 AATTTTGTCTAATGCTTCATAGCAGTGGTAATTCATTCAGTGGTTCAAGAGACAAAAG 120
Db 61 AATTTTGTCTAATGCTTCATAGCAGTGGTAATTCATTCAGTGGTTCAAGAGACAAAAG 120
Qy 121 ATCTCTTTTGTCTGACCAAAATTTCTCACTCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 121 ATCTCTTTTGTCTGACCAAAATTTCTCACTCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Qy 181 GTATTATTATTAATACTGGTATTCAACTGTGTGTAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 181 GTATTATTATTAATACTGGTATTCAACTGTGTGTAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Qy 241 AGAATCTACTGTTATATATCTGGGAGTGTATCAACCAATTCAGCAACTGGCTTCTACT 300
Db 241 AGAATCTACTGTTATATATCTGGGAGTGTATCAACCAATTCAGCAACTGGCTTCTACT 300
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCAACTTTATTTTCTTCCAC 360
Db 301 AGCTCTAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCAACTTTATTTTCTTCCAC 360
Qy 361 TTAAGAGGAGAGTAAAGAGTGTCAATCTGTGTATGTTGTTGGGCTTTCTATTTTGTG 420
Db 361 TTAAGAGGAGAGTAAAGAGTGTCAATCTGTGTATGTTGTTGGGCTTTCTATTTTGTG 420
Qy 421 GCTTGTCACTTTTGTGTATTAACAATGATGAGATTTGGCGGACAAAAGATTTGAAGGA 480
Db 421 GCTTGTCACTTTTGTGTATTAACAATGATGAGATTTGGCGGACAAAAGATTTGAAGGA 480
Qy 481 AACATGACTTGGAAAGATCAAAATTCGAAGTCCAATGTACTTTTCAAAATGACTGTAAACC 540
Db 481 AACATGACTTGGAAAGATCAAAATTCGAAGTCCAATGTACTTTTCAAAATGACTGTAAACC 540
Qy 541 ATGCTAGCAAACTTAGTACCCCTTCACTCTGACCCCTGCTATGTTTGTCTGTATCTGT 600
Db 541 ATGCTAGCAAACTTAGTACCCCTTCACTCTGACCCCTGCTATGTTTGTCTGTATCTGT 600
Qy 601 TCTTTGTGTAAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCGAGC 660
Db 601 TCTTTGTGTAAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCGAGC 660
Qy 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTGTTTATGTCCTATT 720
Db 661 ACCAAGGTCCACATAAAAGCTTTGCAAACTGTGATCTCTCTCTGTTTATGTCCTATT 720
Qy 721 TACTTTCTGTCCATATGATATGATTCAGTTGGAGTTTGGAGTCTCGAAACAAACCTGTC 780
Db 721 TACTTTCTGTCCATATGATATGATTCAGTTGGAGTTTGGAGTCTCGAAACAAACCTGTC 780
Qy 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCACTCTGATT 840
Db 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTCACTCTGATT 840

Db 781 TTCATGTTCTGCAGAGCTATTAGATTACGCTATCTTCAATCCACCCCACTTCATCTCTGATT 840
Qy 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTGTGGCAATAGGTAAGTCTGG 900
Db 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTGTGGCAATAGGTAAGTCTGG 900
Qy 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930
Db 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930

RESULT 15

ADD18119

ID ADD18119 standard; DNA; 971 BP.

XX

AC ADD18119;

XX

15-JAN-2004 (first entry)

XX

Human G-protein coupled receptor (GPCR) DNA sequence Seq IDs.

XX

KW G protein coupled receptor; GPCR; signal transduction pathway; G protein;
KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
KW colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
KW sleeplessness; hypertension; anxiety; stress; renal failure;
KW cardiovascular disorder; neural disorder; oncology disorder;
KW immune disorder; neuroprotective; gene therapy; gene; ds.

XX Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 20..949

FT /*tag= a

FT /product= "Human G-protein coupled receptor"

XX

WO2003016478-A2.

XX

27-FEB-2003.

XX

15-AUG-2002; 2002WO-US026017.

XX

20-AUG-2001; 2001US-0313658P.

PR 12-SEP-2001; 2001US-0318675P.

PR 30-OCT-2001; 2001US-0340703P.

PR 26-NOV-2001; 2001US-0333417P.

PR 06-DEC-2001; 2001US-0338367P.

PR 06-FEB-2002; 2002US-0355596P.

XX

(BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder JN, Ramanathan CS, Gopal S, Mintier GA;

XX

DR WPI; 2003-278558/27.

XX

P-PSDB; ADD18022.

XX

New nucleic acid, useful for manufacturing a medicament for preventing,

PT treating or ameliorating a medical condition e.g., neural disorder.

XX

Example 2; SEQ ID NO 5; 251pp; English.

XX

This invention relates to novel G protein coupled receptors (GPCRs) and

CC their encoding nucleotide sequences. Many medically significant

CC biological processes are mediated by proteins participating in signal

CC transduction pathways involving G proteins. GPCRs are one of the largest

CC receptor superfamilies known. These receptors are biologically important

CC and malfunction of these receptors results in diseases such as

CC Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal

CC pigmentosa and asthma. They are also involved in depression,

CC schizophrenia, sleeplessness, hypertension, anxiety, stress, renal

CC failure and other cardiovascular, neural, oncology and immune disorders.

CC A modulator of the GPCRs of the invention may have neuroprotective

CC activity whilst the sequences of the invention may be useful for gene

CC therapy. The invention may also be useful for manufacturing a medicament

CC for preventing, treating or ameliorating a medical condition. The present
CC sequence is the DNA sequence encoding a human GPCR of the invention.

XX Sequence 971 BP; 251 A; 184 C; 204 G; 332 T; 0 U; 0 Other;
SQ

Query Match 91.6%; Score 851.6; DB 10; Length 971;
Best Local Similarity 94.7%; Pred. No. 7.4e-226;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 ATGATAAAGCTTTTACCCATCATTTTTCAGTCTGTTAGTGGTTTACATTTGTTATTGGA 60
Db 20 ATGACAACTTTTATACCCATCATTTTTCAGTCTGTTAGTGGTTTATTTGTTATTGGA 79

Qy 61 AATTTTGTCTAATGCTTCATAGCACTGTAATTCATTTGATGTTTCAAGAGACAAAAG 120
Db 80 AATTTTGTCTAATGCTTCATAGCACTGTAATTCATTTGATGTTTCAAGAGACAAAAG 139

Qy 121 ATCTCCTTTGCTGACCAAAATTCACCTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG 180
Db 140 ATCTCCTTTGCTGACCAAAATTCACCTGCTCTGGCGGTCTCCAGAGTTGGTTTGTCTGG 199

Qy 181 GTATTATTATAAAGCTGTTTCAACTGTTGTAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 200 GTATTATTATAAAGCTGTTTCAACTGTTGTAATCCAGCTTTTAAATAGTGTAGAAGTA 259

Qy 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCATTTTCAGCAACTGGCTTCTACT 300
Db 260 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCGCCATTTTCAGCAACTGGCTTCTACT 319

Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTTGCCAATTTTCTCAACTTTTATTTTCTTCCAC 360
Db 320 AGCCTCAGCATATTTTATTTGCTCAAGATTTGCCAATTTTCTCAACTTTTATTTTCTTCCAC 379

Qy 361 TTAAGAGGAGAGTTAAGAGTGTCAATCTGTGTGATGTTGTTGGGCCCTTTGCTATTTTGG 420
Db 380 TTAAGAGGAGAGTTAAGAGTGTCAATCTGTGTGATGTTGTTGGGCCCTTTTACTATTTTGG 439

Qy 421 GCTTGTCTATCTTTTGTGATAAACAATGAATCAGAGTTGTCGACAAAAAGAAATTTGAAGA 480
Db 440 GCTTGTCTATCTTTTGTGATAAACAATGAAGAGATTTGACGACAAAGAAATATGAAGA 499

Qy 481 AACATGACTTCGAAGATCAAAATGAAGAGTGCATGTACTTTTCAAAATATGACTGTAAACC 540
Db 500 AACTTGACTTCGAAGATCAAAATGAAGAGTGCAGTGTACTTTTCAGATGCGACTGTAAACC 559

Qy 541 ATGCTAGCAAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTTAATCTGT 600
Db 560 ACCTTAGGAACTTAGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTTAATCTGT 619

Qy 601 TCTTTGTGTAACATCTCAAGAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660
Db 620 TCTCTGTGTAACATCTCAAGAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 679

Qy 661 ACCAAGTCCACATAAAAGCTTTGCAAACTGTGATCTCCTTCTCTTGTATGTGCCATT 720
Db 680 ACCAAGTCCACATAAAAGCTTTGCAAACTGTGATCTTCTTCTCTTGTATGTGCCATT 739

Qy 721 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAGTCTCGGAAACAAACCTGTC 780
Db 740 TACTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAGTCTCGGAAACAAACCTGTC 799

Qy 781 TTCTGTTTCTGCAAGCTATTAGATTACGCTATCTTCAATCCACCCCACTTCATCTCTGATT 840
Db 800 TTCTGTTTCTGCAAGCTATTAGATTACGCTATCTTCAATCCACCCCACTTCATCTCTGATT 859

Qy 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTGTGGCAATAGAGTACTGG 900
Db 860 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTGTGGCAATAGAGTACTGG 919

Qy 901 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 930
Db 920 GTGAAGGAGAGAGAGACTTTCATCTCCATAG 949

Search completed: May 1, 2006, 07:30:18
Job time : 621 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:12:56 ; Search time 140 Seconds
(without alignments)
969.772 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MTFPLPIIFSSILVVFVIG.....FLSVFQWQRYWVGKGTSSP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1 | 1597 | 100.0 | 309 | 5 | AAU11384 | AAU11384 Human T2R |
| 2 | 1597 | 100.0 | 309 | 5 | ABP95936 | ABP95936 Human GPC |
| 3 | 1597 | 100.0 | 309 | 6 | ABP97669 | ABP97669 Amino aci |
| 4 | 1597 | 100.0 | 309 | 6 | ABR58042 | ABR58042 Human GI |
| 5 | 1597 | 100.0 | 309 | 7 | ADC87039 | ADC87039 Human GPC |
| 6 | 1597 | 100.0 | 309 | 8 | ADR29240 | ADR29240 Taste rec |
| 7 | 1575 | 98.6 | 309 | 8 | ADM33295 | ADM33295 Human bit |
| 8 | 1518 | 95.1 | 309 | 9 | ADW74420 | ADW74420 Human bit |
| 9 | 1440 | 90.2 | 309 | 5 | AAU11390 | AAU11390 Human T2R |
| 10 | 1440 | 90.2 | 309 | 6 | ABR58039 | ABR58039 Human GI |
| 11 | 1440 | 90.2 | 309 | 7 | ADC87131 | ADC87131 Human GPC |
| 12 | 1440 | 90.2 | 309 | 8 | ADR29252 | ADR29252 Taste rec |
| 13 | 1440 | 90.2 | 309 | 9 | ADW74596 | ADW74596 Human bit |
| 14 | 1438 | 90.0 | 309 | 9 | ADW74594 | ADW74594 Human bit |
| 15 | 1438 | 90.0 | 309 | 9 | ADW74576 | ADW74576 Human bit |
| 16 | 1427 | 89.4 | 309 | 8 | ADM33297 | ADM33297 Human bit |
| 17 | 1427 | 89.4 | 309 | 9 | ADW74582 | ADW74582 Human bit |
| 18 | 1426 | 89.3 | 309 | 9 | ADW74578 | ADW74578 Human bit |
| 19 | 1424 | 89.2 | 309 | 5 | AAU11386 | AAU11386 Human T2R |
| 20 | 1424 | 89.2 | 309 | 5 | ABP95941 | ABP95941 Human GPC |
| 21 | 1424 | 89.2 | 309 | 6 | ABR58040 | ABR58040 Human GI |
| 22 | 1424 | 89.2 | 309 | 7 | ADC87041 | ADC87041 Human GPC |
| 23 | 1424 | 89.2 | 309 | 7 | ADD18022 | ADD18022 Human G-P |
| 24 | 1424 | 89.2 | 309 | 8 | ADR29244 | ADR29244 Taste rec |

ALIGNMENTS

RESULT 1

AAU11384

ID AAU11384 standard; protein; 309 AA.

XX AC AAU11384;

XX DT 26-MAR-2002 (first entry)

XX DE Human T2R61 (ht2R61) polypeptide.

XX KW Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor;

XX KW ht2R61; T2R61; T2R; bitter taste sensation; taste signalling pathway;

XX KW taste transduction; food taste masking; drug taste masking.

XX OS Homo sapiens.

XX PN WO200177676-A1.

XX PD 18-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010739.

XX PR 07-APR-2000; 2000US-0195532P.

XX PR 13-NOV-2000; 2000US-0247014P.

XX (SENO-) SENOMYX INC.

XX PI Adler JE;

XX WPI; 2002-017486/02.

XX N-PSDB; AAS18167.

Novel isolated mammalian taste cell-specific G protein-coupled receptor, T2R, involved in bitter taste sensation, useful for identifying taste modulators that are used to decrease or mask bitter taste of foods or drugs.

Claim 60; Page 72; 103pp; English.

The invention relates to a mammalian taste cell-specific G protein-coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste sensation. The T2R polypeptides and their associated polynucleotides are useful for screening one or more compounds for the presence of taste detectable by a mammal. Modulators of T2R polypeptides (modulators of taste transduction) are useful for pharmacological and genetic modulations of taste signalling pathways. These modulatory compounds are then used in food and pharmaceutical industries to customise taste, e.g.,

CC to decrease or mask the bitter taste of foods or drugs. This sequence
 CC represents the human T2R61 (hT2R61) polypeptide
 XX
 SQ Sequence 309 AA;

Query Match 100.0%; Score 1597; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 2.2e-152; Indels 0; Gaps 0;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60
 DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLISIFYLKIANFSNFIHL 120
 DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLISIFYLKIANFSNFIHL 120

QY 121 LKRRVKSIVLVMGLGFLFLACHLFLVNNNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180
 DB 121 LKRRVKSIVLVMGLGFLFLACHLFLVNNNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180

QY 181 MVANLVPTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240
 DB 181 MVANLVPTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLKQTFLSVFQWQRYW 300
 DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLKQTFLSVFQWQRYW 300

QY 301 VKGEKTSSP 309
 DB 301 VKGEKTSSP 309

RESULT 2
 ABP95936
 ID ABP95936 standard; protein; 309 AA.
 XX
 AC ABP95936;
 XX
 DT 06-MAR-2003 (first entry)
 XX
 DE Human GPCR polypeptide SEQ ID NO 682.
 XX
 KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KW drug development; gustatory; taste; fragrance; receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200216548-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-IB001446.
 XX
 PR 04-AUG-2000; 2000JP-00237818.
 PR 13-FEB-2001; 2001JP-00034434.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Haga T, Takeda S, Mitaku S;
 XX
 DR WPI; 2002-304118/34.
 DR N-PSDB; AB243210.
 XX
 PT Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX
 XX Claim 10; SEQ ID NO 682; 97pp + Sequence Listing; Japanese.
 PS
 XX The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95936-
 CC

CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 309 AA;

Query Match 100.0%; Score 1597; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 2.2e-152; Indels 0; Gaps 0;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60
 DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRKQISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLISIFYLKIANFSNFIHL 120
 DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLISIFYLKIANFSNFIHL 120

QY 121 LKRRVKSIVLVMGLGFLFLACHLFLVNNNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180
 DB 121 LKRRVKSIVLVMGLGFLFLACHLFLVNNNEIVRTKEFEGNNTWKIKLSAMYFSNMTVT 180

QY 181 MVANLVPTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240
 DB 181 MVANLVPTLTLLSFMLLICSCLKHLKQQLHKGSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLKQTFLSVFQWQRYW 300
 DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLKQTFLSVFQWQRYW 300

QY 301 VKGEKTSSP 309
 DB 301 VKGEKTSSP 309

RESULT 3
 ABP97669
 ID ABP97669 standard; protein; 309 AA.
 XX
 AC ABP97669;
 XX
 DT 16-MAY-2003 (first entry)
 XX
 DE Amino acid sequence of human T2R61 polypeptide.
 XX
 KW Human; T2R4; G protein coupled receptor; GPCR; taste receptor;
 KW bitter alkaloid quinine; denatonium; 6-nitrosaccharin; T2R44; T2R61;
 KW bitter taste; saccharin.
 XX
 OS Homo sapiens.
 XX
 PN WO2003006482-A2.
 XX
 PD 23-JAN-2003.
 XX
 PF 10-JUL-2002; 2002WO-US021602.
 XX
 PR 10-JUL-2001; 2001US-0303811P.
 PR 15-APR-2002; 2002US-0372089P.
 XX
 XX (SENO-) SENOMYX INC.
 XX
 PI Pronin A, Connor J, Tang H, Keung W, Servant G, Adler JB;
 PI O'Connell S, Brust P;
 XX
 DR WPI; 2003-221711/21.

PA (PHLE/) PHLEGER C S W.
XX Walsh JH, Rozengurt JE, Wu SV;
XX WPI: 2003-381713/36.
XX N-PSDB; ACC44478.
XX
XX New nucleic acid encoding a chemosensing G-protein coupled receptor,
XX useful for identifying chemical sensing receptors and signaling molecules
XX that allow pharmacological and genetic modulation of taste transduction
XX pathways.
XX
XX Disclosure; Page 96-97; 101pp; English.
XX
XX This sequence represents a novel isolated chemosensing G-protein coupled
XX receptor (GPCR) from the gastrointestinal tract. The encoding nucleic
XX acid is useful for identifying or isolating chemical sensing receptors
XX (including taste ion channels) and signaling molecules that would allow
XX pharmacological and genetic modulation of taste transduction pathways.
XX The native SRC-1 enteroendocrine cells that naturally express GT2R are
XX useful in identifying modulators of taste receptor-mediated signal
XX transduction. These cells are also used as models for studying taste-
XX mediated signal transduction
XX
XX Sequence 309 AA;
XX
XX Query Match 100.0%; Score 1597; DB 6; Length 309;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-152;
XX Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
XX DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
XX
XX QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFNSNWLATTLISFYLLKIANFSNFIPLH 120
XX DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFNSNWLATTLISFYLLKIANFSNFIPLH 120
XX
XX QY 121 LKERVKSIVLVMLLGPLLFLACHLFVINMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
XX DB 121 LKERVKSIVLVMLLGPLLFLACHLFVINMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
XX
XX QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLCAI 240
XX DB 181 MVANLVPFTLTLLSFMLLICSCLKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLCAI 240
XX
XX QY 241 YFLSIMISVWSFGSLENKPVMECKAIRFSYPSIHPFILLGNKKLKQTFLSVFWQMYW 300
XX DB 241 YFLSIMISVWSFGSLENKPVMECKAIRFSYPSIHPFILLGNKKLKQTFLSVFWQMYW 300
XX
XX QY 301 VKGEKTSSP 309
XX DB 301 VKGEKTSSP 309
XX
XX RESULT 5
XX ADC87039
XX ID ADC87039 standard; protein; 309 AA.
XX
XX AC ADC87039;
XX
XX DT 01-JAN-2004 (first entry)
XX
XX DE Human GPCR protein SEQ ID NO:1492.
XX
XX KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
XX gene therapy.
XX
XX OS Homo sapiens.
XX
XX FN EP1270724-A2.
XX
XX PD 02-JAN-2003.
XX

```

XX 18-JUN-2002; 2002EP-00013517.
XX PF
XX 18-JUN-2001; 2001JP-00246789.
XX PD
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
XX DR N-PSDB; ADC87038.
XX PT New polynucleotide, useful for preparing a composition for treating a
XX patient in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor.
XX PS Claim 2; SEQ ID NO 1492; 28pp; English.
XX CC The invention relates to a novel polynucleotide encoding a guanosine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX the invention may have a use in gene therapy. The polynucleotide and
XX polypeptide are useful for preparing a composition for treating a patient
XX in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor. The protein
XX sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX SQ Sequence 309 AA;
    Query Match      100.0%; Score 1597; DB 7; Length 309;
    Best Local Similarity 100.0%; Pred. No. 2.2e-152;
    Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKQKISFADQILTALAVSRVGLLW 60
DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKQKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLISFYLLKIANFSNFIHL 120
DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLISFYLLKIANFSNFIHL 120
QY 121 LKRRVKSIVLVMGLGPLLFLACHLFVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVMGLGPLLFLACHLFVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLLCAL 240
DB 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLLCAL 240
QY 241 YFLSIMISVWSGSLNKPVEFCKAIRFSYPSIHPFILLWGNKKLKQTFLSVFWMRYW 300
DB 241 YFLSIMISVWSGSLNKPVEFCKAIRFSYPSIHPFILLWGNKKLKQTFLSVFWMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309
RESULT 6
ADR29240
ID ADR29240 standard; protein; 309 AA.
XX ADR29240;
XX AC
XX 04-NOV-2004 (first entry)
XX DT
XX Taste receptor modulation-related human T2R61 protein sequence SeqID179.
XX DE
XX T1R; T2R; taste receptor; G protein; modulatory compound; MAPK activity;
KW CAMP accumulation; adenylyl cyclase; bitter; taste; umami; sweet; T2R61;
KW human.
XX OS Homo sapiens.

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XX WO2004069191-A2.
XX PN
XX 19-AUG-2004.
XX PD
XX 03-FEB-2004; 2004WO-US002987.
XX PF
XX 03-FEB-2003; 2003US-0444172P.
XX PR 26-MAR-2003; 2003US-0457318P.
XX PS (SENO-) SENOMYX INC.
XX PI Servant G, Ozeck M, Brust P, Xu H;
XX WPI; 2004-604341/58.
XX DR N-PSDB; ADR29239.
XX PT Identifying a compound that modulates the activity of a T1R or T2R taste
XX receptor by assaying the effect of the putative modulatory compound on
XX MAPK activation, cAMP accumulation or adenylyl cyclase activity in the
XX eukaryotic cell.
XX PS Disclosure; SEQ ID NO 179; 248pp; English.
XX CC This invention is related to a novel method of identifying a compound
XX that modulates the activity of a T1R or T2R taste receptor. The method
XX comprises providing a eukaryotic cell that expresses a functional T1R or
XX T2R taste receptor and a G protein that couples to it, contacting the
XX eukaryotic cell with a compound and identifying whether the compound
XX modulates the activity of T1R or T2R expressed by the eukaryotic cell
XX based on its effect on MAPK activity, cAMP accumulation or adenylyl
XX cyclase activity. The method is used to identify a compound that blocks or
XX bitter taste associated with a particular T2R activator or that blocks or
XX enhances umami taste elicited by a compound that activates the T1R/T1R3
XX (umami) taste receptor or sweet taste elicited by a compound that
XX activates the T1R2/T1R3 (sweet) taste receptor. The method is useful in
XX identifying a compound that modulates the activity of a T1R or T2R taste
XX receptor. The present sequence is that of a human T2R taste receptor
XX protein which is related to the method of the invention.
XX SQ Sequence 309 AA;
    Query Match      100.0%; Score 1597; DB 8; Length 309;
    Best Local Similarity 100.0%; Pred. No. 2.2e-152;
    Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKQKISFADQILTALAVSRVGLLW 60
DB 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEFWFKQKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLISFYLLKIANFSNFIHL 120
DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATTLISFYLLKIANFSNFIHL 120
QY 121 LKRRVKSIVLVMGLGPLLFLACHLFVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSIVLVMGLGPLLFLACHLFVINNMNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLLCAL 240
DB 181 MVANLVPFTLTLLSFMLLICSCLKHLKKMQLHGKGSQDPSTKVHIKALQTVISFLLLCAL 240
QY 241 YFLSIMISVWSGSLNKPVEFCKAIRFSYPSIHPFILLWGNKKLKQTFLSVFWMRYW 300
DB 241 YFLSIMISVWSGSLNKPVEFCKAIRFSYPSIHPFILLWGNKKLKQTFLSVFWMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309
RESULT 7
ADM33295

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ID ADM33295 standard; protein; 309 AA.
 XX ADM33295;
 AC
 DT 18-NOV-2004 (first entry)
 XX
 DE Human bitter taste receptor TAS2R43 protein SEQ ID NO:9.
 XX
 KW human; bitter taste receptor; food.
 XX
 OS Homo sapiens.
 XX
 PN WO2004029087-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 25-SEP-2003; 2003WO-EP010691.
 XX
 PR 25-SEP-2002; 2002US-0413298P.
 XX
 PA (DEER-) DEUT INST ERNAERUNGSFORSCHUNG POTSDAM.
 XX
 PI Bufo B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;
 XX
 DR WPI; 2004-305149/28.
 DR N-PSDB; ADM33296.
 XX
 PT Novel bitter receptor polynucleotide encoding human TAS2R protein having
 PT bitter substance binding activity, useful for producing nutraceutical or
 PT pharmaceutical compositions comprising antagonists of bitter taste
 PT receptor activity.
 XX
 PS Claim 1; SEQ ID NO 9; 108pp; English.
 XX
 CC The present sequence represents a human bitter taste receptor. Also
 CC described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)
 CC a vector (II) containing (I); (3) a host cell (III) genetically
 CC engineered with (I) or (II); (4) a transgenic non-human animal (IV)
 CC containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino
 CC acid sequence encoded by (I) or obtained by culturing (III) and
 CC recovering polypeptide; (6) an antibody (VI) specifically binding to (V);
 CC (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an
 CC antagonist/inhibitor (VIII) against (V) which is antibody, the
 CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)
 CC isolating (M1) a compound that binds to (V) encoded by (I); (10)
 CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a
 CC foodstuff including human and animal foodstuff, any precursor material or
 CC additive employed in the production of foodstuff comprising (VIII); and
 CC (12) a nutraceutical/pharmaceutical composition comprising (VII); and an
 CC active agent and optionally a carrier. (III) is useful for producing a
 CC polypeptide encoded by (I), which involves culturing (III) and recovering
 CC the polypeptide encoded by (I). (II) is useful for producing cells
 CC capable of expressing at least one of the bitter taste receptor
 CC polypeptide, which involves genetically cells in vitro with (II), where
 CC the bitter taste receptor polypeptide(s) is/are encoded by (I). (M1) or
 CC (M2) can be used for producing food or any precursor material or additive
 CC employed in the production of foodstuffs. (M1) or (M2) can also be used
 CC for producing nutraceutical or pharmaceutical compositions. (I), (II),
 CC (VI) or (VIII) can be used for manufacturing a medicament for the
 CC treatment of an abnormally increased or decreased sensitivity towards a
 CC bitter substance. The identified agonist/inhibitor efficiently suppresses
 CC or eliminated bitter tasting components of food and effectively useful in
 CC food industries.
 XX
 SQ Sequence 309 AA;
 Query Match 98.6%; Score 1575; DB 8; Length 309;
 Best Local Similarity 99.4%; Pred. No. 3.7e-150;
 Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MITFLPIIFSSLVVWTVFVIGNFANGFIALVNSIEFKQKISFADQILTALAVSRVGLLW 60
 DB 1 MITFLPIIFSSLVVWTVFVIGNFANGFIALVNSIEFKQKISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFNSWNLATLTSIFVLLKIANFSNFIPLH 120
 DB 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFNSWNLATLTSIFVLLKIANFSNFIPLH 120
 QY 121 LKRRVKSIVLVMGLGFLFLACHLFFVINNNEIVRTKBEFEGNMTWKIKLSAMYFSNMTVT 180
 DB 121 LKRRVKSIVLVMGLGFLFLACHLFFVINNNEIVRTKBEFEGNMTWKIKLSAMYFSNMTVT 180
 QY 181 MVANLVPPFTLLTSLFMLLICSCKHLKQMLHGKGSQDPSTKVHIKALQTVISFLLLCAL 240
 DB 181 MVANLVPPFTLLTSLFMLLICSCKHLKQMLHGKGSQDPSTKVHIKALQTVISFLLLCAL 240
 QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLINGNKKLKQTFVSVFQWQRYW 300
 DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLINGNKKLKQTFVSVFQWQRYW 300
 QY 301 VKGKTSSTP 309
 DB 301 VKGKTSSTP 309
 RESULT 8
 ADM74420
 ID ADM74420 standard; protein; 309 AA.
 XX
 AC ADM74420;
 DT 07-APR-2005 (first entry)
 XX
 DE Human bitter taste receptor protein T2R43 with an encoded SNP Seq 32.
 XX
 KW receptor; SNP detection; SAP; single amino acid polymorphism; screening;
 KW DNA microarray; flavor enhancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 35
 FT /label= Trp, Ser
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 90
 FT /label= Val
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 154
 FT /label= Arg, Gly
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 170
 FT /label= Ser, Arg
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 200
 FT /label= Cys, Phe
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 212
 FT /label= Arg, His
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 221
 FT /label= Thr
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 294
 FT /label= Phe, Leu
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 295
 FT /label= Trp, Arg
 FT /note= "Encoded by a single nucleotide polymorphism"
 FT Misc-difference 297
 FT /label= Met, Val
 FT /note= "Encoded by a single nucleotide polymorphism"
 PN WO2005007891-A2.
 XX 27-JAN-2005.
 PD
 XX

```

PF 18-JUN-2004; 2004WO-US019489.
XX
XX
PR 19-JUN-2003; 2003US-0480035P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Drayna D, Kim U;
PI
XX WPI; 2005-152091/16.
DR N-PSDB; ADW74419.
XX
XX New isolated bitter taste receptor (T2R) variant-specific nucleic acid
PT molecule comprises at least 10 contiguous nucleotides, useful for
PT defining large groups of populations who perceive bitter tastes
PT differently.
XX
XX Claim 18; SEQ ID NO 32; 567pp; English.
XX
XX This invention relates to novel human bitter taste receptor (T2R) variant
CC -specific nucleic acid molecules, each spanning at least one SNP
CC identified in the specification. Specifically, it refers to the T2R
CC allele nucleic acid molecules and the encoded proteins thereof. The
CC present invention describes a method of screening compounds useful for
CC modulating bitter taste and using a specific binding agent that is
CC capable of discriminating between two or more polypeptides. Accordingly,
CC it provides a method of determining the T2R genotype of a subject using
CC at least one oligonucleotide from each T2R haplotype/allele on a
CC microarray to identify T2R single nucleotide polymorphisms. As such, the
CC isolated T2R variant-specific nucleic acid molecules are useful in the
CC development of flavorings and flavor enhancers as it can be used to
CC define large groups of populations who perceive bitter tastes
CC differently. It is also used to identify compounds that interact
CC differently with different variants of a taste receptor. This polypeptide
CC sequence is a bitter taste receptor T2R protein of the invention.
XX
SQ Sequence 309 AA;
Query Match 95.1%; Score 1518; DB 9; Length 309;
Best Local Similarity 96.8%; Pred. No. 2.1e-144; Mismatches 10; Indels 0; Gaps 0;
Matches 299; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 MITFLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
DB 1 MITFLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
DB 61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAXINHFSNWLATLSIFYLKIANFSNFIPLH 120
QY 121 LKRRVKSVLVLMGLPLFLACHLFVINNMNEIVTRKEEGNMTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSVLVLMGLPLFLACHLFVINNMNEIVTRKEEGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPPTLTLLSFMLLITCSLCKHLKKMQLXGKSGQDPSTKVHIKALQTVISFLLCAI 240
DB 181 MVANLVPPTLTLLSFMLLITCSLCKHLKKMQLXGKSGQDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300
DB 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309
RESULT 9
ID AAU11390
XX AAU11390 standard; protein; 309 AA.
XX AC AAU11390;
XX
DT 26-MAR-2002 (first entry)

```

```

XX Human T2R75 (ht2R75) polypeptide.
DE
XX Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor;
KW ht2R75; T2R75; T2R; bitter taste sensation; taste signalling pathway;
KW taste transduction; food taste masking; drug taste masking.
XX
XX Homo sapiens.
XX
XX WO200177676-A1.
XX
XX 18-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US010739.
PF
XX 07-APR-2000; 2000US-0195532P.
PR 13-NOV-2000; 2000US-0247014P.
XX (SENO-) SENOMYX INC.
PA
XX Adler JE;
PI
XX WPI; 2002-017486/02.
DR N-PSDB; AAS18173.
XX
XX Novel isolated mammalian taste cell-specific G protein-coupled receptor,
PT T2R, involved in bitter taste sensation, useful for identifying taste
PT modulators that are used to decrease or mask bitter taste of foods or
XX drugs.
XX
XX Claim 60; Page 75; 103pp; English.
XX
XX The invention relates to a mammalian taste cell-specific G protein-
CC coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste
CC sensation. The T2R polypeptides and their associated polynucleotides are
CC useful for screening one or more compounds for the presence of taste
CC detectable by a mammal. Modulators of T2R polypeptides (modulators of
CC taste transduction) are useful for pharmacological and genetic
CC modulations of taste signalling pathways. These modulatory compounds are
CC then used in food and pharmaceutical industries to customise taste, e.g.,
CC to decrease or mask the bitter taste of foods or drugs. This sequence
CC represents the human T2R75 (ht2R75) polypeptide
XX
SQ Sequence 309 AA;
Query Match 90.2%; Score 1440; DB 5; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.5e-136;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;
QY 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
DB 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
DB 61 VLLLNWYSTVLNPAFNSIEVRTAYNVWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
QY 121 LKRRVKSVLVLMGLPLFLACHLFVINNMNEIVTRKEEGNMTWKIKLSAMYFSNMTVT 180
DB 121 LKRRVKSVLVLMGLPLFLACHLFVINNMNEIVTRKEEGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPPTLTLLSFMLLITCSLCKHLKKMQLXGKSGQDPSTKVHIKALQTVISFLLCAI 240
DB 181 ILANLVPPTLTLLSFMLLITCSLCKHLKKMQLXGKSGQDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFQMRYW 300
DB 241 YFLSIMISVWSFGSLENKPVFMFCEATAFSPSTHPFILIWGNKKLKQTFLSVLMHVRVY 300
QY 301 VKGEKTS 308
DB 301 VKGEKPS 308

```

RESULT 10
 ABR58039 standard; protein; 309 AA.
 ID ABR58039 standard; protein; 309 AA.
 XX
 AC ABR58039;
 XX
 DT 25-JUL-2003 (first entry)
 XX
 DE Human GI endocrine cell specific GPCR GT2R-h54.
 XX
 KW Chemosensor; G-protein coupled receptor; GPCR; receptor; ion channel;
 KW gastrointestinal tract; taste; enteroendocrine cell.
 XX
 OS Homo sapiens.
 XX
 WO2003031604-A1.
 XX
 PN 17-APR-2003.
 XX
 PD 11-OCT-2002; 2002WO-US032664.
 XX
 PF 12-OCT-2001; 2001US-0328993P.
 XX
 PR (REGC) UNIV CALIFORNIA.
 XX
 PA (PHLE/) PHLEGER C S W.
 XX
 PI Walsh JH, Rozengurt JE, Wu SV;
 XX
 DR WPI; 2003-381713/36.
 XX
 DR N-PSDB; ACC44475.
 XX
 XX New nucleic acid encoding a chemosensing G-protein coupled receptor,
 PT useful for identifying chemical sensing receptors and signaling molecules
 PT that allow pharmacological and genetic modulation of taste transduction
 PT pathways.
 XX
 PS Disclosure; Page 92-93; 101pp; English.
 XX
 CC This sequence represents a novel isolated chemosensing G-protein coupled
 CC receptor (GPCR) from the gastrointestinal tract. The encoding nucleic
 CC acid is useful for identifying or isolating chemical sensing receptors
 CC (including taste ion channels) and signaling molecules that would allow
 CC pharmacological and genetic modulation of taste transduction pathways.
 CC The native STC-1 enteroendocrine cells that naturally express GPCR are
 CC useful in identifying modulators of taste receptor-mediated signal
 CC transduction. These cells are also used as models for studying taste-
 CC mediated signal transduction
 XX
 SQ Sequence 309 AA;
 Query Match 90.2%; Score 1440; DB 6; Length 309;
 Best Local Similarity 88.3%; Pred. No. 1.5e-136;
 Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;
 Qy 1 MITFLPIIFSSLVVVTFTVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60
 Db 1 MITFLPIIFSSILVVTFTVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60
 Qy 61 VLLNNWYSTVLNPAFNSVEVRTTAYNIWAVINHFNSNWLATTLSIFYLLKIANFSNFIPLH 120
 Db 61 VLVLNWTATELNPAFNSIEVRITAYNVAVINHFNSNWLATSLSIFYLLKIANFSNLIPLH 120
 Qy 121 LKRRVKSIVLMLGLPLLFLACHLFPVINNNEIVRTKEFGNMTWKIKLSAMYFSNMTVT 180
 Db 121 LKRRVKSIVLILVGLPLLFLVCHLFPVINNQIIITWKEYEGNMTWKIKLSAMYLNTTVT 180
 Qy 181 MVANLVPFTLTLSFMILLICSLCKHKKMQLHGKSGQDPSKVIKALQTVISFLLCAI 240
 Db 181 ILANLVPFTLTLSFLLILICSLCKHKKMQLHGKSGQDPSKVIKALQTVISFLLCAI 240
 Qy 241 YFTSIMITSVNSFSGLENKPVFMFCKAIRPSYSPHIFLLIWNKKLKQTFLSVFMQRYW 300
 Db 241 YFTSIMITSVNSFSGLENKPVFMFCKAIRPSYSPHIFLLIWNKKLKQTFLSVFMQRYW 300

CC differently. It is also used to identify compounds that interact
CC differently with different variants of a taste receptor. This polypeptide
CC sequence is a bitter taste receptor T2R haplotype protein that contains
CC single amino acid polymorphisms encoded by DNA that features SNPs of the
CC invention.

XX Sequence 309 AA;

SQ Query Match 90.2%; Score 1440; DB 9; Length 309;

Best Local Similarity 88.3%; Pred. No. 1.5e-136;

Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSILVVTFTVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

Db 1 MITFLPIIFSSILVVTFTVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTLVNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFVLLKIANFSNFIPLH 120

Db 61 VLVLNWYATELNPAFNSIEVRITAYNVAVINHFSNWLATLSIFVLLKIANFSNLIPLH 120

QY 121 LKRRVKSIVLVMGLPFLFLACHLFVNNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

Db 121 LKRRVKSIVLVMGLPFLFLACHLFVNNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

QY 181 MYANLVPPFTLTLLSFMLLICSCKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

Db 181 ILANLVPPFTLTLLSFMLLICSCKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

QY 241 YFLSIMISVWSFSGLENKPVFMFCKAIRFSYPSIHPFILLIWNKKNLQTFLSVFWQMRVW 300

Db 241 YFLSIMISVWSFSGLENKPVFMFCKAIRFSYPSIHPFILLIWNKKNLQTFLSVFWQMRVW 300

QY 301 VKGEKTSS 308

Db 301 VKGEKPSS 308

RESULT 14

ADW74594

ID ADW74594 standard; protein; 309 AA.

AC ADW74594;

XX 07-APR-2005 (first entry)

XX Human bitter taste receptor haplotype protein t2R46 Seq 206.

XX receptor; SNP detection; SAP; single amino acid polymorphism; screening;

XX DNA microarray; flavor enhancer.

XX Homo sapiens.

XX WO2005007891-A2.

XX 27-JAN-2005.

XX 18-JUN-2004; 2004WO-US019489.

XX 19-JUN-2003; 2003US-0480035P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Drayna D, Kim U;

XX WPI; 2005-152091/16.

XX N-PSDB; ADW74593.

XX New isolated bitter taste receptor (T2R) variant-specific nucleic acid

XX molecule comprises at least 10 contiguous nucleotides, useful for

XX defining large groups of populations who perceive bitter tastes

XX differently.

XX Claim 18; SEQ ID NO 206; 567pp; English.

XX

CC This invention relates to novel human bitter taste receptor (T2R) variant

CC -specific nucleic acid molecules, each spanning at least one SNP

CC identified in the specification. Specifically, it refers to the T2R

CC allele nucleic acid molecules and the encoded proteins thereof. The

CC present invention describes a method of screening compounds useful for

CC modulating bitter taste and using a specific binding agent that is

CC capable of discriminating between two or more polypeptides. Accordingly,

CC it provides a method of determining the T2R genotype of a subject using

CC at least one oligonucleotide from each T2R haplotype/allele on a

CC microarray to identify T2R single nucleotide polymorphisms. As such, the

CC isolated T2R variant-specific nucleic acid molecules are useful in the

CC development of flavorings and flavor enhancers as it can be used to

CC define large groups of populations who perceive bitter tastes

CC differently. It is also used to identify compounds that interact

CC differently with different variants of a taste receptor. This polypeptide

CC sequence is a bitter taste receptor T2R haplotype protein that contains

CC single amino acid polymorphisms encoded by DNA that features SNPs of the

XX invention.

SQ Sequence 309 AA;

Query Match 90.0%; Score 1438; DB 9; Length 309;

Best Local Similarity 88.0%; Pred. No. 2.4e-136;

Matches 271; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSILVVTFTVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

Db 1 MITFLPIIFSSILVVTFTVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTLVNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFVLLKIANFSNFIPLH 120

Db 61 VLVLNWYATELNPAFNSIEVRITAYNVAVINHFSNWLATLSIFVLLKIANFSNLIPLH 120

QY 121 LKRRVKSIVLVMGLPFLFLACHLFVNNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

Db 121 LKRRVKSIVLVMGLPFLFLACHLFVNNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

QY 181 MYANLVPPFTLTLLSFMLLICSCKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

Db 181 ILANLVPPFTLTLLSFMLLICSCKHLKQMLHKGSGQDPSTKVHIKALQTVISFLLLCAL 240

QY 241 YFLSIMISVWSFSGLENKPVFMFCKAIRFSYPSIHPFILLIWNKKNLQTFLSVFWQMRVW 300

Db 241 YFLSIMISVWSFSGLENKPVFMFCKAIRFSYPSIHPFILLIWNKKNLQTFLSVFWQMRVW 300

QY 301 VKGEKTSS 308

Db 301 VKGEKPSS 308

RESULT 15

ADW74576

ID ADW74576 standard; protein; 309 AA.

AC ADW74576;

XX 07-APR-2005 (first entry)

XX Human bitter taste receptor haplotype protein T2R44 Seq 188.

XX receptor; SNP detection; SAP; single amino acid polymorphism; screening;

XX DNA microarray; flavor enhancer.

XX Homo sapiens.

XX WO2005007891-A2.

XX 27-JAN-2005.

XX 18-JUN-2004; 2004WO-US019489.

XX 19-JUN-2003; 2003US-0480035P.

C:Species: Homo sapiens (man)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C:Accession: I30435
R:O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Teui, L.; Kennedy, J.L.; Shi, X.; Petri
Gene 136, 355-360, 1993
A:Title: A human gene that shows identity with the gene encoding the angiotensin receptor
A:Reference number: I30435, MUID:94124031, PMID:8294032
A:Accession: I30435
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-380 <RES>
A:Cross-references: UNIPROT:P35414; UNIPARC:UPI0000001622; EMBL:U03642; NID:G425351; PID
C:Genetics:
A:Gene: APJ
A:Map position: 11q12
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin

Query Match 8.2%; Score 130.5; DB 2; Length 380;
Best Local Similarity 19.0%; Pred. No. 0.0036;
Matches 66; Conservative 79; Mismatches 125; Indels 77; Gaps 16;

QY 8 IPSSLVVTVFVIGNFANGFIALVNSIEW----FKRQKISFADQILTALAVSRVGLLWLL 63
DB 30 LIPAIYMLVFLGTTGNGLVL-----WTVPRSSREKRSADIFTASLAVA--DLTFVVT 81
QY 64 LNWYSTV----LNPAPNSVEVTTAYNIWAVINHSNMLATLSIF--YLLKIANFSNFI 117
DB 82 LPLMATYTRYDWDWPGFTGFKLSSYLIF--VNMVASVFLTGLSFDRLAIVRVAN-- 137
QY 118 FLHLKRRVKSIVLMLGLPL-LFLACHLFI--NMNEIVRTKEFGNM-----T 163
DB 138 -ARLRVSGAVATAVLWLAALLAMPVNVVLTGDTGENTKVCQMYDSVAVTVSSWA 196
QY 164 WKIKLSAMVFNMTVTVMANLVPTLLSPMLLICSRLKHLKKQHLKSGSDPSTKV 223
DB 197 MEVGL-----GVSSSTTVGVVPTIMLTVCYFFIAQTIAHFRKERIEG----- 239
QY 224 HIKALQTVISFLLLCALYF-----LSIMISVWSFGSLENKP-----VFMECKAIR 268
DB 240 -LRKERRLLSIIVLVVTFALCWPMPYHLVKTLYMLGLSLHLWPCDFLFLMNIFFYCTCIS 298
QY 269 FSPYGIHPILLWGNKKLKQTFSLVF--WQMR-----YVWKGKETS 308
DB 299 YVNSCLNPLFYAFPPRFRQACTSMCCQSRCACTSHSSGKSKAS 345

RESULT 3
H82889
conserved hypothetical UUA450 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: H82889
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: H82889
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <GLA>
A:Cross-references: UNIPARC:UPI00000C1C70; GB:AE002141; GB:AF222894; NID:G6899434; PIDN
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UU450
A:Genetic code: SGC3
C:Superfamily: uncharacterized conserved protein

Query Match 7.9%; Score 126.5; DB 2; Length 387;
Best Local Similarity 21.4%; Pred. No. 0.0077;
Matches 77; Conservative 70; Mismatches 108; Indels 105; Gaps 18;

QY 1 MITFLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLIW 60

DB 25 IVCLLMIIISILFILDID--DFQNLFIKINSLKTIK-----LAILW 63
QY 61 VLLLNWYSTVLPNAPNSVEVTTAYNIWAVINHSN-----WLATLSIFYLLKIAN 112
DB 64 LLIL-----ISPFIFFAFMFIVIAVDTYKNQIKIAWKKWILYSFSLIFLNAVTP 113
QY 113 FS-----NFIFL-----HLKRRVKSIVLML-----LGPLLFLACHLFIWNNNEIVRTKE 157
DB 114 FVGSEPPSIYFLNKNQYHNLKVSALLVSSSTFYELGQVIVTPSPFIYINIELI----- 168
QY 158 PEGNNTWKIKLSAM--YFSNMTVTMANLVPTLLSFM-----LIICS----- 201
DB 169 -----TYAVNNTSLPFFYLLAVGIADL---CMTAIYFVLGSKLHFRSVLYNNVK 220
QY 202 ---LCKHLKRWQLHKGSGSDPSTKV-----HIKALQTVISFLLLCALYFSLMISW-SFG 253
DB 221 KLFKLVLTKTIELIQKNQNISFKAFVLYYEFTLRVSLLAFAVIGVWYNIGIYALMYISYR 280
QY 254 SLENKVPFMFCKAIRFSYPSI-----HPILLWGNKKLKQTFSLVFW-----QMRV---WV 301
DB 281 LVEPKPHNIPFDL--FNYTNIAVTATNPVLPFGSEGSQFMRVFLTDNQIRIAMNWL 338

RESULT 4
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CR-4
C:Species: Homo sapiens (man)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; v
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cl
A:Reference number: A57160; MUID:95370289; PMID:7642634
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: UNIPROT:P51679; UNIPARC:UPI000002DFE9; GB:X85740; NID:gl370103; PID
A:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:76-97/Domain: transmembrane #status predicted <TM1>
F:113-133/Domain: transmembrane #status predicted <TM2>
F:151-175/Domain: transmembrane #status predicted <TM3>
F:208-264/Domain: transmembrane #status predicted <TM4>
F:243-264/Domain: transmembrane #status predicted <TM5>
F:291-308/Domain: transmembrane #status predicted <TM6>
F:29-276,110-187/disulfide bonds: #status predicted <TM7>
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predict
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 7.7%; Score 123; DB 2; Length 360;
Best Local Similarity 18.5%; Pred. No. 0.014;
Matches 63; Conservative 62; Mismatches 105; Indels 110; Gaps 14;

QY 4 FLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKI-SFADQILTALAVS----- 54
DB 41 FLPLFLYS-----LVFVGLLGNSSVVVLV---LFYKRLRSMTDVLNLAISDILLFVPSL 92
QY 55 -----RVGLL-----WYLLNWSYTLNPAFNSVEVRTAYNIWAVINHSN 97
DB 93 FPGVYAADQWVFLGLCKMISWMLVGVFGYGFVFMMSID-----RYLAIVHAVPSL 146
QY 98 LATTLSIFYLLKIANFSNFIHLKRRVKSIVLWMLGLPLFLACHLFIWNNNEIVRTKE 157

Db 147 RARTLTGYVITSLATWSAVFASLP-----GFLFSTC--YTERNHYYCKTKY 191
Qy 158 PEGNWTWIKLKLSAMVFSNMVTVMANLVFPFTLLSFMLLCSL--CKHLKMKQLHGKG 215
Db 192 SLNSTYTKV-----LSLENIILGLVPIGIMLFCVSMIIRTLQHCNEKN----- 238
Qy 216 SODPSTKVHIKALQTVISPLLC-----AIYFLSIMISVMSFGSLENKPVFMFC--- 264
Db 239 -----KAVKMFVAVVLFLGFWTPYNIIVLETLVEL-----EVLQDCTFE 279
Qy 265 -----KAIRSYSIHPFILLWGNKKLQTFLSVF 294
Db 280 RYLDVAIOATETLAFVHCCNLPIIYFFLGEXKPKRYLOLF 319

RESULT 5
A70346
conserved hypothetical protein aq_509 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A70346
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: A70346
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-441 <AQF>
A:Cross-references: UNIPROT:O66797; UNIPARC:UPI0000056398; GB:AE000693; NID:g2983148; PI
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_509

Query Match 7.5%; Score 120.5; DB 2; Length 441;
Best Local Similarity 22.2%; Pred. No. 0.027;
Matches 76; Conservative 55; Mismatches 134; Indels 77; Gaps 16;
Qy 7 IIPSSLVVTVFVIGNFANGFTALVNSIEWFKRKQISFADQILTALAVSERVGLWVLLNW 66
Db 105 LLFTPTLLTGLTGLAIGFPFVLKI-----PVGFNNEALSYTQVAYFLLLPYLLPNF 158
Qy 67 YSTVLNPAFNSVVRTTAYNTWAVINHF-----SNMLATTLSIFYLKIANF 113
Db 159 LFHFEGAVLSVR-RFTYVFGFELFSFPLFPLGLFLFYKWLVLPLSLISFAQIATL 217
Qy 114 SNFI-----FLH-----LKRKRVSVILVMLLGLPFLFLACHLFINNNEIVRTKEFGNMTWK 165
Db 218 YMFYVGRFHIHNFPLNQTTKILNHFYLSALYGVHLF-----IVIDRAF-GSLIGE 270
Qy 166 IKLKSAVFSNMVTVMANLVFPFTLLSFMLLCSLCK-HLKQQLHGKSGQDPSTKVH 224
Db 271 -KSISAIHYG-----LIVASIPRGIRLENIAITLSKSGDKIKLNF-----Y 313
Qy 225 IKALQTVISFLLCAIYFLSIMIS-VMSFGSLENKPVFMFCIAIRFSYPSIHPFLLIWG- 282
Db 314 IKRILIVSGISLLAPFPFAEIIIVKLLFGYGAFTQMDLITVETATRF-YLSLPLFMFLWPI 372
Qy 283 -----NKKLQKQTF-----LSVFW--QMRYVWVG 303
Db 373 LYRVFQIKENLKPVFIAISGITVNGILNYPFVLKLNYGIGK 414

RESULT 6
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: JC4587
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HO>
A:Cross-references: UNIPROT:P51680; UNIPARC:UPI0000028F3B; EMBL:X90862; NID:g1167851; PI
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4

C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,483,194/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 7.3%; Score 117; DB 2; Length 360;
Best Local Similarity 22.0%; Pred. No. 0.042;
Matches 51; Conservative 44; Mismatches 75; Indels 62; Gaps 10;
Qy 4 FLPIFSSLVVTVFVIGNFANGFTALVNSIEWFKRKQISFADQILTALAVS----- 54
Db 41 FLPLPLYS-----LVFLGLGFGSVVVLV--LPKYKELK-SMTDVLNLAISDLLFLVLSLP 93
Qy 55 -----RVGLL-----WVLLNMYSTVLNPAFNSVVRTTAYNIWAVINHFNSWL 98
Db 94 FWGYVAAQDQWVFLGLCKIVSMVYLVGYSGIFFIMLSID-----RYLAIVHAVFSLK 147
Qy 99 ATTLSIFVLKIANFSPIFLHKKRVKSVILVMLLGLPFLFLACHLFINNNEIVRTKEF 158
Db 148 ARTLTGYVITSLTWSAVFASLP-----GLLFSTC--YTEHNHYCKTKQYS 192
Qy 159 EGNMTWIKLKLSAMVFSNMVTVMANLVFPFTLLSFMLLCSL--CKHLK 208
Db 193 VNSTWKV-----LSSLEINVLGLIPLIGIMLFWYSMIIRTLQHCNEKK 237

RESULT 7
S69659

hypothetical protein YDR492w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 31-Dec-2004
C:Accession: S69659; S69664
R:Dieckrich, F.S.
submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae coemids 9410, 8035, 8166, and 9787.
A:Reference number: S69554

A:Accession: S69659
A:Molecule type: DNA
A:Residues: 1-316 <DIE>
A:Cross-references: UNIPROT:Q03419; UNIPARC:UPI000006B9A1; EMBL:U33050; NID:g927726; PID
C:Genetics:
A:Gene: MIPS:YDR492w
A:Map position: 4R
C:Superfamily: Adiponectin receptor protein and homologs

Query Match 7.3%; Score 116.5; DB 2; Length 316;
Best Local Similarity 21.1%; Pred. No. 0.04;
Matches 45; Conservative 39; Mismatches 66; Indels 63; Gaps 8;
Qy 150 NEIVRTKEFGNMTWIKLKLSAMVFSNMVTVMANLVF-----FTLLSFMFL----- 197
Db 53 NDKILTGVVRETLSWKKCLYSLFYNNETVNIIVLPAIVYFVFAITLTNYFLIPVPPS 112
Qy 198 -----LICSCLKHLKQQLHGKSGQDPSTKVHIKALQTVISFLLLC 238
Db 113 TWSDDYTVINIFLMGAFSCLMSSCFHC--MKQHSKQSNFWSKLDYLGIIISLSCMIP 170
Qy 239 AIYV-LSIMISVMSFGSLENKPVFMFCIAI-----RFSYPSIHP---FLLIWG----- 282
Db 171 IYFGYFDHISYLSLFTVITVLATFTCTVCLVHDKFTSTPRPRAMPFFILFGSGLLPL 230
Qy 283 -----NKKLQKQTFLSVFMQRYWVG 303

Db 223 GSHLCVSLFYGSATL-----VFYCSSVLHSTHKKMIASLWYTVISPLNPF 269
Qy 278 ILIWNKKLQKTFLSV 294
Db 270 IYSLRNKDVKGALGKLF 286
RESULT 13
T32241
hypothetical protein T15B7.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32241
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T15B7.
A:Reference number: Z21139
C:Accession: T32241
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-355 <PAU>
A:Cross-references: UNIPROT:O17029; UNIPARC:UPI000007FF98; EMBL:AF022985; PIDN:AAB69970.
A:Experimental source: strain Bristol N2; clone T15B7
C:Genetics:
A:Gene: CESP-T15B7.11
A:Map position: 5
A:Introns: 36/2; 103/2; 150/2; 185/2; 219/3; 255/2; 295/2

Query Match 7.0%; Score 112; DB 2; Length 355;
Best Local Similarity 24.7%; Pred. No. 0.1;
Matches 74; Conservative 48; Mismatches 88; Indels 90; Gaps 16;
Qy 8 IFSSLVVTFTVGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVGL-----LWVLL 63
Db 45 LLSSLIVFSF-----FANLILIVLS---HKEMRHSGINVMFIAVSDFGCAVTGLMOLF 97
Qy 64 LNWYSTVLNPAFNSVEVRTAY-----NIWAVINHFSN-WLATTLSIFLLKIANFSNFI 117
Db 98 IRNYS-----DQWMLFATLQFVDYLAVFHASLFLAAGWALCRVMAL-NFSN-- 147
Qy 118 FHLKRRKRS---VILVMLLGPLLFLACHLFLVNNNEIVRTKEFE-----GNM 162
Db 148 ---RLXDKWQSPRYALRVTCVAVITVLTSLVPVNEVKTTDDGEVITDTSFLAYGCL 205
Qy 163 TWKIKLKSAMYSNNMTVTWVANLVPTLTLLSFMLLICSLKHLKMKQLHGKSGQDPSTX 222
Db 206 LMKIVL-----VFGICFPLIPCTLMLLLSILL-----LQKMD-EGKRSSVPINR 249
Qy 223 VHKK-----ALQTVISFLLCAL-----YF--LSIMISVWSF 252
Db 250 NHHKRVQDLDRSSQLTIQILIVFLITEVPGQVFSIGGIEVDYLYNQNLTFIMWVLSF 309

RESULT 14
T39009
hypothetical protein SPAC6B12.02c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39009
R:Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z21815
C:Accession: T39009
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1888 <GEN>
A:Cross-references: UNIPROT:O14207; UNIPARC:UPI000013AA2F; EMBL:Z98531; PIDN:CAB11064.1;
A:Experimental source: strain 972h-; cosmid c6B12
C:Genetics:
A:Gene: SPDB:SPAC6B12.02c
A:Map position: 1
C:Superfamily: Schizosaccharomyces hypothetical protein SPAC6B12.02c

Query Match 7.0%; Score 112; DB 2; Length 1888;
Best Local Similarity 19.2%; Pred. No. 0.56;
Matches 75; Conservative 59; Mismatches 128; Indels 128; Gaps 19;
Qy 1 MITPLPIFFSLVVV---TFVIGNFANGFIALVNSIEWFKRKISFADQILTALAVSRVG 57
Db 801 LVEKIAVLVFTQVVFYCEFGELGNQN-----INKVSLA-----SDLISKLLSAGOSG 849
Qy 58 LLWVLLLNWYSTVLNPAFNSVEVRTAYNIWAVINHFSNWLATTLSIFLLKIANFSNP- 116
Db 850 -----LLECYRNLRIOASDTTVIDTFLFLESNLIH-----LFHYVKKYKALWEQVN 897
Qy 117 IFLHLKRRVKSVI-----LVMLLGPLLFLACHLFLVNNNEIVRTKEFGNMT-WKIKL 168
Db 898 SFFDLQKKELSILEMEKIWYVIMTLNP-----VFQIGLN---GTTTSPGNNSEWPLII 947
Qy 169 KSA-----MYFSNNMTVTWVANLVPTLTLLSFM-----LICSICLHKKMQ 210
Db 948 RVSESAFQKHKGDNVKKVVERYLRTVFLRIHFLISEWEDVAQILFLIPDFFSHRKEND 1007
Qy 211 LHGKSGQDPST-----KVHICALQTVISFLLLCALYFLSLMI----- 247
Db 1008 LSSSISEDTPTDFDFVKSLDRPPNHLVLTALDT-----CFVIYLVKILISISLRQVD 1060
Qy 248 -----SVWSFGSILENKPVEMFC---KAIRFSYPSIHPF 277
Db 1061 ENTNSIKRIVSRLOPLHSRQVTRSPFSIKDFMSLEHTHTLLICLYWAAPENCRPSLNRI 1120
Qy 278 --ILIWGNKKLKQTFLSV-FW--QMRVWK 302
Db 1121 RDIVVDNSHLKARLISLKAMLHLMKYVIK 1150

RESULT 15
148261
angiotensin II receptor type 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 148261; JC2028
R:Horiuchi, M.; Koike, G.; Yamada, T.; Mukoyama, M.; Nakajima, M.; Dzau, V.J.
J. Biol. Chem. 270, 20225-20230, 1995
A:Title: The growth-dependent expression of angiotensin II type 2 receptor is regulated
A:Reference number: 148261; MUID:95378283; PMID:7650042
A:Accession: 148261
A:Status: translation not shown; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-363 <RES>
A:Cross-references: UNIPROT:P35374; UNIPARC:UPI000000185D; EMBL:U11073; NID:g607834; PID
B:Nakajima, M.; Mukoyama, M.; Pratt, R.E.; Horiuchi, M.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 197, 393-399, 1993
A:Title: Cloning of cDNA and analysis of the gene for mouse angiotensin II type 2 receptor
A:Reference number: JC2028; MUID:94092107; PMID:8267573
A:Accession: JC2028
A:Molecule type: mRNA
A:Residues: 1-363 <NAK>
A:Cross-references: UNIPARC:UPI000000185D; GB:U04828; NID:g439862; PIDN:AACS2128.1; PID:
C:Comment: This protein is the biologically active peptide of the renin-angiotensin syst
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:46-71/Domain: transmembrane #status predicted <TM1>
F:81-102/Domain: transmembrane #status predicted <TM2>
F:120-140/Domain: transmembrane #status predicted <TM3>
F:161-179/Domain: transmembrane #status predicted <TM4>
F:209-234/Domain: transmembrane #status predicted <TM5>
F:257-278/Domain: transmembrane #status predicted <TM6>
F:286-313/Domain: transmembrane #status predicted <TM7>
F:4.13,24,29,34/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:79,152,348,353,354/Binding site: phosphate (Ser) (covalent) #status predicted
F:346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.0%; Score 111.5; DB 2; Length 363;
Best Local Similarity 20.7%; Pred. No. 0.12;

```
Matches 69; Conservative 65; Mismatches 132; Indels 67; Gaps 17;
Qy 5 LPIIFSSLVVTVFVIGNFANGFIAL-----VNSIEWFKRQKISFADQIILTALAV 53
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
47 IPVLY-----YMIFVIG-FAVNIWVWSLFCQKQPKVSSIYIF---NLALADLLLLATLP 98
Qy 54 SRVGLLWVLLNW-YSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLSIFYL--LKI 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
99 -----LMATYYSRYDWFEGP-----VMCKVFGSFLTLNMPA-----SIFFITCMV 140
Qy 111 ANFSNFIPLHLKRRVKS-----VILVMLLGPLLFLACHLFVINMNEIVRTKEFEENMTW 164
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141 DRYQSVIYFPLSQRRNPWQASVYVPLWCMACLSSLPTFP-----RDVRTIEYLGWNAC 195
Qy 165 KIKLSAMYFS-NMTVTWVANLVPPFTLLSFMLLICSCLKHLKQMLHGKG--SQDPST 221
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 IMAFPPEKYAOWSAGIALMKNILGFIIPLIATCYFGIRKHLKKTNSYGKNRITRDQVL 255
Qy 222 KVHIKALQTVISFLLLCALYP--LSMISVWSFGSLENKPVFM-----FCKAIRFSYP 272
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 KM---AAAVVLAF-IICWLPFHVLTFLDALTWGIIINSCEVIAVIDLALPFAILLGFTNS 311
Qy 273 SIHPFILLWGNKKLQTFPLSVFMQRYVYVKGK 305
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
312 CVNPFYCYGVGNRFQOKLRSVFRVPIITWLQGR 344
```

Search completed: April 27, 2006, 21:19:35
Job time : 43 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:13:26 ; Search time 166 Seconds
(without alignments)
1313.303 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MITFLPIFFSLVVFVIG.....FLSVFMQRYVWVGKGTSP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------------|--------------------|
| 1 | 1579 | 98.9 | 309 | 1 T2R43_PANTR | Q646b4 pan troglod |
| 2 | 1578 | 98.8 | 309 | 1 T2R43_PANPA | Q5Y500 pan paniscu |
| 3 | 1575 | 98.6 | 309 | 1 T2R43_HUMAN | P59537 homo sapien |
| 4 | 1575 | 98.6 | 309 | 2 Q645X4_HUMAN | Q645x4 homo sapien |
| 5 | 1489 | 93.2 | 290 | 2 Q5UG21_PANTR | Q5UG21 pan troglod |
| 6 | 1463 | 91.6 | 285 | 2 Q50KJ2_HUMAN | Q50Kj2 homo sapien |
| 7 | 1453 | 91.0 | 309 | 1 T2R44_PANPA | Q646e0 pan paniscu |
| 8 | 1450 | 90.8 | 285 | 2 Q50KJ1_PANTR | Q50Kj1 pan troglod |
| 9 | 1448 | 90.7 | 309 | 1 T2R44_PANTR | Q646b9 pan troglod |
| 10 | 1440 | 90.2 | 309 | 1 T2R46_HUMAN | P59540 homo sapien |
| 11 | 1427 | 89.4 | 309 | 1 T2R44_HUMAN | P59538 homo sapien |
| 12 | 1427 | 89.4 | 309 | 1 T2R46_PANPA | Q646e1 pan paniscu |
| 13 | 1419 | 88.9 | 309 | 1 T2R44_PONPY | Q645v3 pongo pygma |
| 14 | 1418 | 88.8 | 309 | 1 T2R46_PANTR | Q646c0 pan troglod |
| 15 | 1412 | 88.4 | 309 | 1 T2R46_GORGO | Q645z7 gorilla gor |
| 16 | 1411 | 88.4 | 309 | 1 T2R46_PANPA | Q5Y4z8 pan paniscu |
| 17 | 1405 | 88.0 | 309 | 1 T2R66_PANPA | Q5Y4y8 pan paniscu |
| 18 | 1396 | 87.4 | 309 | 1 T2R44_GORGO | Q645z6 gorilla gor |
| 19 | 1394 | 87.3 | 296 | 2 Q5UG24_PANTR | Q5UG24 pan troglod |
| 20 | 1382 | 86.5 | 309 | 1 T2R44_PAPHA | Q646f9 papio hamad |
| 21 | 1361.5 | 85.3 | 308 | 1 T2R43_PAPHA | Q646f8 papio hamad |
| 22 | 1359.5 | 85.1 | 308 | 1 T2R43_MACMU | Q645t3 macaca mula |
| 23 | 1335 | 83.6 | 299 | 1 T2R45_HUMAN | P59539 homo sapien |
| 24 | 1335 | 83.6 | 299 | 2 Q50KH4_MACMU | Q50Kh4 macaca mula |
| 25 | 1334 | 83.5 | 285 | 2 Q50KH0_HUMAN | Q50Kh0 homo sapien |
| 26 | 1333 | 83.5 | 298 | 2 Q50KH5_MACMU | Q50Kh5 macaca mula |
| 27 | 1332 | 83.4 | 285 | 2 Q50KH1_HUMAN | Q50Kh1 homo sapien |
| 28 | 1318 | 82.5 | 319 | 2 Q64528_9PRIM | Q64528 gorilla gor |
| 29 | 1317 | 82.5 | 319 | 1 T2R47_PONPY | Q645v4 pongo pygma |
| 30 | 1311 | 82.1 | 285 | 2 Q50KG8_PANTR | Q50Kg8 pan troglod |
| 31 | 1309 | 82.0 | 319 | 1 T2R47_PANTR | Q646c1 pan troglod |

RESULT 1

| ID | T2R43_PANTR | STANDARD; | PRT; | 309 AA. |
|----|---|-----------|------|---------|
| AC | Q646B4; | | | |
| DT | 01-FEB-2005 (Rel. 46, Created) | | | |
| DT | 01-FEB-2005 (Rel. 46, Last sequence update) | | | |
| DT | 10-MAY-2005 (Rel. 47, Last annotation update) | | | |
| DE | Taste receptor type 2 member 43 (T2R43). | | | |
| GN | Name=TAS2R43; | | | |
| OS | Pan troglodytes (Chimpanzee). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; | | | |
| OC | Pan. | | | |
| OX | NCBI_TaxID=9598; | | | |
| RN | [1] | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RX | PubMed=15496349; DOI=10.1093/molbev/msi027; | | | |
| RA | Fischer A., Gilad Y., Man O., Paabo S.; | | | |
| RL | "Evolution of bitter taste receptors in humans and apes."; | | | |
| RL | Mol. Biol. Evol. 22:432-436(2005). | | | |
| CC | -1- FUNCTION: Receptor that may play a role in the perception of bitterness and is gustducin-linked. May play a role in sensing the chemical composition of the gastrointestinal content. The activity of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 activation and lead to the gating of TRPM5 (By similarity). | | | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein. | | | |
| CC | -1- MISCELLANEOUS: Most taste cells may be activated by a limited number of bitter compounds; individual taste cells can discriminate among bitter stimuli. | | | |
| CC | -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family. | | | |
| CC | ----- | | | |
| CC | This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. | | | |
| CC | ----- | | | |
| CC | EMBL; AY724889; AAU21105.1; -; Genomic_DNA. | | | |
| CC | InterPro; IPR007960; TAS2_recept. | | | |
| DR | PANTHER; PTHR11394; TAS2_recept; 1. | | | |
| DR | Pfam; PF05296; TAS2R; 1. | | | |
| KW | G-protein coupled receptor; Glycoprotein; Receptor; | | | |
| KW | Sensory transduction; Taste; Extracellular (Potential). | | | |
| FT | TOPO_DOM 1 1 | | | |
| FT | TOPO_DOM 2 22 | | | |
| FT | TOPO_DOM 23 46 | | | |
| FT | TRANSMEM 47 67 | | | |
| FT | TOPO_DOM 68 86 | | | |
| FT | TRANSMEM 87 107 | | | |
| FT | TOPO_DOM 108 126 | | | |
| FT | TRANSMEM 127 147 | | | |
| FT | TOPO_DOM 148 178 | | | |
| FT | TRANSMEM 179 199 | | | |
| FT | TOPO_DOM 200 229 | | | |

ALIGNMENTS

Q646g0 papio hamad
Q646e2 pan paniscu
Q50ki4 hylobates a
P59541 homo sapien
Q645t4 macaca mula
Q50kg9 pan troglod
Q50ki1 pan troglod
Q50ki7 trachypithe
Q50ki0 gorilla gor
Q5xu77 macaca mula
Q50ki2 homo sapien
Q50ki9 macaca mula
Q50kj0 macaca mula
Q50kg4 pongo pygma

32 1306 81.8 309 1 T2R46_PAPHA
33 1304 81.7 319 1 T2R47_PANPA
34 1295 81.1 272 2 Q50KI4_HYLAG
35 1293 81.0 319 1 T2R47_HUMAN
36 1292.5 80.9 308 1 T2R46_MACMU
37 1292 80.9 285 2 Q50KG9_PANTR
38 1291 80.8 285 2 Q50KI1_PANTR
39 1290 80.8 285 2 Q50KI7_TRACR
40 1286 80.5 285 2 Q50KI0_9PRIM
41 1283.5 80.4 285 2 Q5XU77_MACMU
42 1278 80.0 285 2 Q50KI2_HUMAN
43 1273 79.7 285 2 Q50KI9_MACMU
44 1272 79.6 285 2 Q50KJ0_MACMU
45 1270 79.5 296 2 Q50KG4_PONPY

FT TRANSMEM 230 250 6 (Potential).
 FT TOPO DOM 251 259 Extracellular (Potential).
 FT TRANSMEM 260 280 7 (Potential).
 FT TOPO DOM 281 309 Cytoplasmic (Potential).
 FT CARBOHYD 161 161 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 176 176 N-linked (GlcNAc. .) (Potential).
 SQ SEQUENCE 309 AA; 35612 MW; 504332C099242D52 CRC64;

Query Match 98.9%; Score 1579; DB 1; Length 309;
 Best Local Similarity 98.4%; Pred. No. 9.9e-108;
 Matches 304; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
 Db 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFNSFIPLH 120
 Db 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFNSFIPLH 120

QY 121 LKRRVKSUILVMLLGPLLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMVT 180
 Db 121 LKRRVKSUILVMLLGPLLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMVT 180

QY 181 MVANLVPFTLLSFMILLICSLCKHLKQMLHGKSGQDPSTKVHKAQTIVISFLLCAI 240
 Db 181 MVANLVPFTLLSFMILLICSLCKHLKQMLHGKSGQDPSTKVHKAQTIVISFLLCAI 240

QY 241 YFLSIMISVWFSGLSENKPVFMFCKAIRFSYPSIHPFILINGNKKLKQTFILSVFQMRYW 300
 Db 241 YFLSIMISVWFSGLSENKPVFMFCKAIRFSYPSIHPFILINGNKKLKQTFILSVFQMRYW 300

QY 301 VKGEKTSPP 309
 Db 301 VKGEKTSPP 309

RESULT 2

T2R43 PANPA
 ID T2R43 PANPA STANDARD; PRT; 309 AA.
 AC Q5Y500;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Taste receptor type 2 member 43 (T2R43).
 GN Name=TA52R43;
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pan.
 OX NCBI_TaxID=9597;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15466715; DOI=10.1073/pnas.0404894101;
 RA Parry C.M., Erkner A., le Coutre J.;
 RT "Divergence of T2R chemosensory receptor families in humans, bonobos, and chimpanzees";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14830-14834 (2004).
 CC -!- FUNCTION: Receptor that may play a role in the perception of bitterness and is gustducin-linked. May play a role in sensing the chemical composition of the gastrointestinal content. The activity of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 activation and lead to the gating of TRPM5 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited number of bitter compounds; individual taste cells can discriminate among bitter stimuli.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
 CC -----
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CC removed.
 CC EMBL; AY677147; AAV28575.1; -; Genomic_DNA.
 DR InterPro; IPR007960; TAS2_recept.
 DR PANTHER; PTHR11394; TAS2_recept; 1.
 DR Pfam; PF05296; TAS2R; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor;
 KW Sensory transduction; Taste; Transducer; Transmembrane.
 FT TOPO DOM 1 1 Extracellular (Potential).
 FT TRANSMEM 2 22 1 (Potential).
 FT TOPO DOM 23 46 Cytoplasmic (Potential).
 FT TRANSMEM 47 67 2 (Potential).
 FT TOPO DOM 68 86 Extracellular (Potential).
 FT TRANSMEM 87 107 3 (Potential).
 FT TOPO DOM 108 126 Cytoplasmic (Potential).
 FT TRANSMEM 127 147 4 (Potential).
 FT TOPO DOM 148 178 Extracellular (Potential).
 FT TRANSMEM 179 199 5 (Potential).
 FT TOPO DOM 200 229 Cytoplasmic (Potential).
 FT TRANSMEM 230 250 6 (Potential).
 FT TOPO DOM 251 259 Extracellular (Potential).
 FT TRANSMEM 260 280 7 (Potential).
 FT TOPO DOM 281 309 Cytoplasmic (Potential).
 FT CARBOHYD 161 161 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 176 176 N-linked (GlcNAc. .) (Potential).
 SQ SEQUENCE 309 AA; 35611 MW; A4F4DPE412C4DD99 CRC64;

Query Match 98.8%; Score 1578; DB 1; Length 309;
 Best Local Similarity 98.4%; Pred. No. 1.2e-107;
 Matches 304; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
 Db 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFNSFIPLH 120
 Db 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFNSFIPLH 120

QY 121 LKRRVKSUILVMLLGPLLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMVT 180
 Db 121 LKRRVKSUILVMLLGPLLFLACHLFPVNNNEIVRTKEFGNMTWKIKLSAMYFSNMVT 180

QY 181 MVANLVPFTLLSFMILLICSLCKHLKQMLHGKSGQDPSTKVHKAQTIVISFLLCAI 240
 Db 181 MVANLVPFTLLSFMILLICSLCKHLKQMLHGKSGQDPSTKVHKAQTIVISFLLCAI 240

QY 241 YFLSIMISVWFSGLSENKPVFMFCKAIRFSYPSIHPFILINGNKKLKQTFILSVFQMRYW 300
 Db 241 YFLSIMISVWFSGLSENKPVFMFCKAIRFSYPSIHPFILINGNKKLKQTFILSVFQMRYW 300

QY 301 VKGEKTSPP 309
 Db 301 VKGEKTSPP 309

RESULT 3
 T2R43 HUMAN
 ID T2R43 HUMAN STANDARD; PRT; 309 AA.
 AC P59537; P59546;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Taste receptor type 2 member 43 (T2R43) (T2R52).
 GN Name=TA52R43;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22297730; PubMed=12379855; DOI=10.1038/ng1014;

RA Bufo B., Hofmann T., Krautwurst D., Raguse J.-D., Meyerhof W.;
RT "The human TAS2R16 receptor mediates bitter taste in response to beta-
RL glucopyranosides.";
RN Nat. Genet. 32:397-401(2002).
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22471936; PubMed=12584440; DOI=10.1159/000068546;
RX Conte C., Ebeling M., Marcuz A., Nef P., Andres-Barquin P.J.;
RA "Identification and characterization of human taste receptor genes
RT belonging to the TAS2R family.";
RL Cytogenet. Genome Res. 98:45-53(2002).
RN [3]
RP REVIEW.
RX MEDLINE=22135574; PubMed=12139982; DOI=10.1016/S0959-4388(02)00345-8;
RA Montmayeur J.-P., Matsunami H.;
RT "Receptors for bitter and sweet taste.";
RL Curr. Opin. Neurobiol. 12:366-371(2002).
RN [4]
RP REVIEW.
RX MEDLINE=21634924; PubMed=11695554; DOI=10.1074/jbc.R100054200;
RA Margolskee R.F.;
RT "Molecular mechanisms of bitter and sweet taste transduction.";
RL J. Biol. Chem. 277:1-4(2002).
RN [5]
RP REVIEW.
RX MEDLINE=22469025; PubMed=12581520; DOI=10.1016/S0092-8674(03)00071-0;
RA Zhang Y., Hoon M.A., Chandrasekar J., Mueller K.L., Cook B., Wu D.,
RA Zuker C.S., Ryba N.J.;
RT "Coding of sweet, bitter, and umami tastes: different receptor cells
RT sharing similar signaling pathways.";
RL Cell 112:293-301(2003).
RN [6]
RP ACTIVATION BY SACCCHARIN AND ACESULFAME K.
RX PubMed=15537898; DOI=10.1523/JNEUROSCI.1225-04.2004;
RA Kuhn C., Bufo B., Winnig M., Hofmann T., Frank O., Behrens M.,
RA Leutschenko T., Slack J.P., Ward C.D., Meyerhof W.;
RT "Bitter taste receptors for saccharin and acesulfame K.";
RL J. Neurosci. 24:10260-10265(2004).
CC -1- FUNCTION: Receptor that may play a role in the perception of
CC bitterness and is gustducin-linked. May play a role in sensing the
CC chemical composition of the gastrointestinal content. The activity
CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC activation and lead to the gating of TRPM5 (by similarity).
CC Activated by the sulfonyl amide sweeteners saccharin and
CC acesulfame K.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
CC of the tongue and exclusively in gustducin-positive cells.
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
CC discriminate among bitter stimuli.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF494237; AAM19328.1; -; Genomic DNA.
CC EMBL; AY14089; AAM63539.1; -; Genomic DNA.
CC Ensembl; ENSG00000184291; Homo sapiens.
CC HGNC; HGNC:18875; TAS2R43.
CC InterPro; IPR007960; TAS2_recept.
CC PANTHER; PTHR11394; TAS2_recept; 1.
CC Pfam; PF05296; TAS2R; 1.
CC G-protein coupled receptor; Glycoprotein; Receptor;
KW Sensory transduction; Taste; Transducer; Transmembrane.
FT TOPO_DOM 1 1
FT TRANSMEM 2 22
FT TOPO_DOM 23 46
FT TRANSMEM 47 67
FT TOPO_DOM 68 86
FT TRANSMEM 68 86

FT TRANSMEM 87 107 3 (Potential).
FT TOPO_DOM 108 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT TOPO_DOM 148 178 Extracellular (Potential).
FT TRANSMEM 179 199 5 (Potential).
FT TOPO_DOM 200 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT TOPO_DOM 251 259 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO_DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).
FT CONFLICT 35 35 S -> W (in Ref. 2).
FT CONFLICT 212 212 R -> H (in Ref. 2).
SQ SEQUENCE 309 AA; 679B67259C609FD1 CRC64;
Query Match 98.6%; Score 1575; DB 1; Length 309;
Best Local Similarity 99.4%; Pred. No. 2e-107; Indels 0; Gaps 0;
Matches 307; Conservative 0; Mismatches 2;
QY 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
Db 1 MITFLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVETTAIYNIWAVINHFNSNWLATLISIPYLKIANFSFIPLH 120
Db 61 VLLLNWYSTVLNPAFNSVEVETTAIYNIWAVINHFNSNWLATLISIPYLKIANFSFIPLH 120
QY 121 LKRRVKSVILVMLGPLLFLACHLFPVNMNIEIVRTKBEFEGNMTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSVILVMLGPLLFLACHLFPVNMNIEIVRTKBEFEGNMTWKIKLSAMYFSNMTVT 180
QY 181 MVANLVPTLTLLSFMLLICSCLKHLKQMLHGKSGQDPSTKVKHIKALQTVISFLLLCAL 240
Db 181 MVANLVPTLTLLSFMLLICSCLKHLKQMLHGKSGQDPSTKVKHIKALQTVISFLLLCAL 240
QY 241 YFLSIMISVWSFGSLNKPVMFCKAIRFSPSIHPFILIWGNKKLKQTFILSVFQMWRYW 300
Db 241 YFLSIMISVWSFGSLNKPVMFCKAIRFSPSIHPFILIWGNKKLKQTFILSVFQMWRYW 300
QY 301 VKGEKTSPP 309
Db 301 VKGEKTSPP 309
RESULT 4
Q645X4 HUMAN PRELIMINARY; PRT; 309 AA.
AC Q645X4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Taste receptor T2R43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496549; DOI=10.1093/molbev/msi027;
RA Fischer A., Gilad Y., Man O., Paabo S.;
RT "Evolution of bitter taste receptors in humans and apes.";
RL Mol. Biol. Evol. 22:432-436(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Anne F., Yoav G., Orna M., Svante P.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY724943; AAU21145.1; -; Genomic DNA.
KW Receptor.
SQ SEQUENCE 309 AA; 35518 MW; 679B67259C609FD1 CRC64;
Query Match 98.6%; Score 1575; DB 2; Length 309;

Best Local Similarity 99.4%; Pred. No. 2e-107; Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MITPLPIIFSSLVVTVFVIGNPANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
 DB 1 MITPLPIIFSSLVVTVFVIGNPANGFIALVNSIESFKRQKISFADQILTALAVSRVGLLW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120
 DB 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLVMGLGFLPLACHLFLVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180
 DB 121 LKRRVKSIVLVMGLGFLPLACHLFLVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVT 180

QY 181 MYANLVPPFTLLSFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
 DB 181 MYANLVPPFTLLSFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YPLSTMISVWSGSLNKPVMFCKAIRFSYPSIHPFILWGNKKLKQTFLSVFWQMYW 300
 DB 241 YPLSTMISVWSGSLNKPVMFCKAIRFSYPSIHPFILWGNKKLKQTFLSVFWQMYW 300

QY 301 VKGKTSPP 309
 DB 301 VKGKTSPP 309

RESULT 5
 Q5UG21 PANTR PRELIMINARY; PRT; 290 AA.
 AC Q5UG21 PANTR PRELIMINARY; PRT; 290 AA.
 DT 01-FEB-2005 (TremBLrel. 29, Created)
 DT 01-FEB-2005 (TremBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TremBLrel. 29, Last annotation update)
 DE Candidate bitter taste receptor TAS2R43 (Fragment).
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 EX PubMed:15367488; DOI=10.1093/hmg/ddh289;
 RA Wang X., Thomas S.D., Zhang J.;
 RT "Relaxation of selective constraint and loss of function in the evolution of human bitter taste receptor genes."
 RL Hum. Mol. Genet. 13:2671-2678(2004).
 DR EMBL; AY736059; AAU47352.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR GO; GO:0050909; P:perception of taste; IEA.
 DR InterPro; IPR007960; TAS2_recept.
 DR PANTHER; PTHR11394; TAS2_Recept.
 DR Pfam; PF05296; TAS2R; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 290
 SQ SEQUENCE 290 AA; 33390 MW; BB8D30AF746C46CC CRC64;

Query Match 93.2%; Score 1489; DB 2; Length 290;
 Best Local Similarity 99.3%; Pred. No. 3.6e-101; Matches 288; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 SSVLVVTVFVIGNPANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLWLLNWTST 69
 DB 1 SSVLVVTVFVIGNPANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLWLLNWTST 60

QY 70 VLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSVI 129
 DB 61 VLNPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSVI 120

QY 130 LVMLLGPFLFLACHLFLVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVTWVANLVPP 189
 DB 130 LVMLLGPFLFLACHLFLVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVTWVANLVPP 180

QY 190 LTLISFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFSLMISV 249
 DB 181 LTLISFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFSLMISV 240

QY 250 WSPGSLNKPVMFCKAIRFSYPSIHPFILWGNKKLKQTFLSVFWQMY 299
 DB 241 WSPGSLNKPVMFCKAIRFSYPSIHPFILWGNKKLKQTFLSVFWQMY 290

RESULT 6
 Q50KJ2 HUMAN PRELIMINARY; PRT; 285 AA.
 AC Q50KJ2 HUMAN PRELIMINARY; PRT; 285 AA.
 DT 13-SEP-2005 (TremBLrel. 31, Created)
 DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
 DE Bitter taste receptor T2R43 (Fragment).
 GN Name=Hosa (Biaka) -T2R43;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Go Y., Satta Y., Takahata O., Takahata N.;
 RT "Lineage-Specific Loss of Function of Bitter Taste Receptor Genes in Humans and Nonhuman Primates."
 RL Genetics 170:313-326(2005).
 DR EMBL; AB199182; BAD98056.1; -; Genomic DNA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 285
 SQ SEQUENCE 285 AA; 32657 MW; 36880236D179A620 CRC64;

Query Match 91.6%; Score 1463; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.9e-99; Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FSSLVVTVFVIGNPANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLWLLNWTST 68
 DB 1 FSSLVVTVFVIGNPANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLWLLNWTST 60

QY 69 TVLPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSV 128
 DB 61 TVLPAFNSVEVRTTAYNIWAVINHFSNWLATLSIFYLKIANFSNFIPLHKKRVKSV 120

QY 129 ILVMLLGPFLFLACHLFLVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVTWVANLVPP 188
 DB 121 ILVMLLGPFLFLACHLFLVINNNEIVRTKEFEGNMTWKIKLSAMYFSNMTVTWVANLVPP 180

QY 189 TLTLSFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFSLMIS 248
 DB 181 TLTLSFMLLICSCKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFSLMIS 240

QY 249 WSPGSLNKPVMFCKAIRFSYPSIHPFILWGNKKLKQTFLSV 293
 DB 241 WSPGSLNKPVMFCKAIRFSYPSIHPFILWGNKKLKQTFLSV 285

RESULT 7
 T2R44 PANPA STANDARD; PRT; 309 AA.
 ID T2R44 PANPA STANDARD; PRT; 309 AA.
 AC Q646E0; Q51429;
 DT 01-FEB-2005 (Rel. 46, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Taste receptor type 2 member 44 (T2R44).
GN Name=TAS2R44;
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9597;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496549; DOI=10.1093/molbev/msi027;
RA Fischer A., Gilad Y., Man O., Paabo S.;
RT "Evolution of bitter taste receptors in humans and apes.";
RL Mol. Biol. Evol. 22:432-436(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15466715; DOI=10.1073/pnas.0404894101;
RA Parry C.M., Erkner A., le Coutre J.;
RT "Divergence of T2R chemosensory receptor families in humans, bonobos,
and chimpanzees.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14830-14834(2004).
CC -!- FUNCTION: Receptor that may play a role in the perception of
bitterness and is gustducin-linked. May play a role in sensing the
chemical composition of the gastrointestinal content. The activity
of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
activation and lead to the gating of TRPM5 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited
number of bitter compounds; individual taste cells can
discriminate among bitter stimuli.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC -----
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use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC ENBL; AY724849; AAU21079.1; -; Genomic DNA.
DR EMBL; AY677148; AAU28576.1; -; Genomic DNA.
DR InterPro; IPR007960; TAS2_recept.
DR PANTHER; PTHR11394; TAS2_recept.
DR Pfam; PF05296; TAS2R; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor;
KW Sensory transduction; Taste; Transducer; Transmembrane.
FT TOPO_DOM 1 2 Extracellular (Potential).
FT TRANSMEM 3 23 1 (Potential).
FT TOPO_DOM 24 55 Cytoplasmic (Potential).
FT TRANSMEM 56 76 2 (Potential).
FT TOPO_DOM 77 100 Extracellular (Potential).
FT TRANSMEM 101 121 3 (Potential).
FT TOPO_DOM 122 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT TOPO_DOM 148 181 Extracellular (Potential).
FT TRANSMEM 182 202 5 (Potential).
FT TOPO_DOM 203 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT TOPO_DOM 251 259 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO_DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
FT CONFLICT 5 5 L -> I (in Ref. 2).
FT CONFLICT 116 116 F -> L (in Ref. 2).
SQ SEQUENCE 309 AA; 35357 MW; 5E15295BBD59A7AA CRC64;
Query Match 91.0%; Score 1453; DB 1; Length 309;
Best Local Similarity 90.9%; Pred. No. 1.7e-98;
Matches 281; Conservative 11; Mismatches 17; Indels 0; Gaps 0;
QY 1 MITLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60
DB 1 MTTLPIIFSSLVVTVFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLH 120

Db 61 VLLLNWYSTVLNPAFNSVEVTRTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLH 120
QY 121 LKRRVKSVLLVMLGPKLLFLACHLPVNNMNEIVRTKPEGNMTWKIKLKSAWYFSNMTVT 180
Db 121 LKRRVKSVLLVMLGPKLLFLACHLPVNNMNEIVRTKPEGNMTWKIKLKSAWYFSNMTVT 180
QY 181 MVANLVPTTLTLLSFMLLICSCLKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
Db 181 TLGNLVPTTLTLLCFLLLICSCLKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
QY 241 YFLSIMISVWSFGSLENKPVMPCKAIRFSPSHPPFLIINGNKKLKOTFLSVFQMRYW 300
Db 241 YFLSIMISVWSFGSLENKPVMPCKAIRFSPSHPPFLIINGNKKLKOTFLSVLRQVRVY 300
QY 301 VKGEKTSPP 309
Db 301 VKGEKTSPP 309
RESULT 8
Q50KJ1_PANTR PRELIMINARY; PRT; 285 AA.
ID Q50KJ1_PANTR PRELIMINARY; PRT; 285 AA.
AC Q50KJ1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Bitter taste receptor T2R43 (Fragment).
GN Name=Patr-T2R43;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Go Y., Satta Y., Takenaka O., Takahata N.;
RT "Lineage-Specific Loss of Function of Bitter Taste Receptor Genes in
Humans and Nonhuman Primates.";
RL Genetics 170:313-326(2005).
DR EMBL; AB199183; BAD98057.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
FT NON_TER 1 1
FT NON_TER 285 285
SQ SEQUENCE 285 AA; 32597 MW; 40EF9BDDC6418FF4 CRC64;
Query Match 90.8%; Score 1450; DB 2; Length 285;
Best Local Similarity 98.6%; Pred. No. 2.6e-98;
Matches 281; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 9 FSSLVVTVFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLWLLLNWYS 68
Db 1 FSSLVVTVFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLWLLLNWYS 60
QY 69 TVLNPAFNSVEVTRTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLHKKRVKSV 128
Db 61 TVLNPAFNSVEVTRTAYNIWAVINHFNSNWLATLSIFYLLKIANFSNFIPLHKKRVKSV 120
QY 129 ILVNLGPKLLFLACHLPVNNMNEIVRTKPEGNMTWKIKLKSAWYFSNMTVTWVANLVPP 188
Db 121 ILVNLGPKLLFLACHLPVNNMNEIVRTKPEGNMTWKIKLKSAWYFSNMTVTWVANLVPP 180
QY 189 TLLTSLFMLLICSCLKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFLSIMIS 248
Db 181 TLLTSLFMLLICSCLKHLKKMQLHGKSGQDPSTKVHIKALQTVISFLLCAIYFLSIMIS 240
QY 249 VWSFGSLENKPVMPCKAIRFSPSHPPFLIINGNKKLKOTFLSV 293
Db 241 VWSFGSLENKPVMPCKAIRFSPSHPPFLIINGNKKLKOTFLSV 285
RESULT 9

CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
 CC activation and lead to the gating of TRPM5 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
 CC of the tongue and exclusively in gustducin-positive cells.
 CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited
 CC number of bitter compounds; individual taste cells can
 CC discriminate among bitter stimuli.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AV114091; AAM63541.1; -; Genomic DNA.
 CC EMBL: AV724941; AU21143.1; -; Genomic DNA.
 CC EMBL: AF494227; AAM19318.1; -; Genomic DNA.
 CC DR Ensembl: ENSG00000184861; Homo sapiens.
 CC DR HGNC: HGNC:18877; TAS2R46.
 CC DR InterPro: IPR007960; TAS2_recept.
 CC DR PANTHER: PTHR11394; TAS2_recept; 1.
 CC DR Pfam: PF05296; TAS2R; 1.
 CC KW G-protein coupled receptor; Glycoprotein; Receptor;
 KW Sensory transduction; Taste; Transducer; Transmembrane.
 FT TOPO_DOM 1 1 Extracellular (Potential).
 FT TRANSMEM 2 22 1 (Potential).
 FT TOPO_DOM 23 46 Cytoplasmic (Potential).
 FT TRANSMEM 47 67 2 (Potential).
 FT TOPO_DOM 68 86 Extracellular (Potential).
 FT TRANSMEM 87 107 3 (Potential).
 FT TOPO_DOM 108 126 Cytoplasmic (Potential).
 FT TRANSMEM 127 147 4 (Potential).
 FT TOPO_DOM 148 178 Extracellular (Potential).
 FT TRANSMEM 179 199 5 (Potential).
 FT TOPO_DOM 200 229 Cytoplasmic (Potential).
 FT TRANSMEM 230 250 6 (Potential).
 FT TOPO_DOM 251 259 Extracellular (Potential).
 FT TRANSMEM 260 280 7 (Potential).
 FT TOPO_DOM 281 309 Cytoplasmic (Potential).
 FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 228 228 L -> M (in Ref. 2).
 FT CONFLICT 296 297 HV -> QM (in Ref. 3).
 SQ SEQUENCE 309 AA; 35523 MW; FF4D7747F0CE47EF CRC64;
 Query Match 90.2%; Score 1440; DB 1; Length 309;
 Best Local Similarity 88.3%; Pred. No. 1.5e-97;
 Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MITPLPIFSSLIWVTFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60
 Db 1 MITPLPIFSSLIWVTFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLW 60
 QY 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIAVINHFSNWLATLISIFYLKIANFSNFIHL 120
 Db 61 VLVLNWYATFLNPAFNSIEVRITAYNVAVINHFSNWLATLSIFYLKIANFSNFIHL 120
 QY 121 LKRRKSVILVMLGLPLFLACHLFWINNEIVRKEFGNNTWKLSAMVFSNMTVT 180
 Db 121 LKRRKSVVLVTLGLPLFLVCHLFWINNNQIWTKEYEGNNTWKLSAMVLSNNTVT 180
 QY 181 MVANLVPTLTLSFLMLLCSLCKHLKQMLGKGSQDPSTKVHIALQTIVISFLLLCAL 240
 Db 181 ILIANLVPTLTLSIFLLILCSLCKHLKQMLGKGSQDPSTKVHIALQTIVISFLLLCAL 240
 QY 241 YFLSIMISVMSGSLNKPVMFCIAIRPSYPSIHPFILLGNKKLKQTFLSVFQMRYW 300
 Db 241 YFLSIIMSVMSPESLENKVPVNFCEAIFSYSTHPPFILLGNKKLKQTFLSVLHVRYW 300
 QY 301 VKGEKTS 308
 |||||

Db 301 VKGEXPSS 308
 RESULT 11
 T2R44 HUMAN STANDARD; PRT; 309 AA.
 ID P59538; P59547; Q645X5;
 AC 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Taste receptor type 2 member 44 (T2R44) (T2R53).
 GN Name=TAS2R44; (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22297730; PubMed=12379855; DOI=10.1038/ng1014;
 RA Bufo B., Hofmann T., Krautwurst D., Rague J.-D., Meyerhof W.;
 RT "The human TAS2R16 receptor mediates bitter taste in response to beta-glucopyranosides";
 RL Cytogenet. Genome Res. 98:45-53 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22471936; PubMed=12584440; DOI=10.1159/000068546;
 RA Conte C., Ebbling M., Marcuz A., Nef P., Andres-Barquin P.J.;
 RT "Identification and characterization of human taste receptor genes belonging to the TAS2R family";
 RL Cytogenet. Genome Res. 98:45-53 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496549; DOI=10.1093/molbev/msi027;
 RA Fischer A., Gilad Y., Man O., Paabo S.;
 RT "Evolution of bitter taste receptors in humans and apes";
 RL Mol. Biol. Evol. 22:432-436 (2005).
 RN [4]
 RP REVIEW.
 RX MEDLINE=22135574; PubMed=12139982; DOI=10.1016/S0959-4388(02)00345-8;
 RA Montmayeur J.-P., Matsunami H.;
 RT "Receptors for bitter and sweet taste";
 RL Curr. Opin. Neurobiol. 12:366-371 (2002).
 RN [5]
 RP REVIEW.
 RX MEDLINE=21634924; PubMed=11696554; DOI=10.1074/jbc.R100054200;
 RA Margolske R.F.;
 RT "Molecular mechanisms of bitter and sweet taste transduction";
 RL J. Biol. Chem. 277:1-4 (2002).
 RN [6]
 RP REVIEW.
 RX MEDLINE=22469025; PubMed=12581520; DOI=10.1016/S0092-8674(03)00071-0;
 RA Zhang Y., Hoon M.A., Chandrasekar J., Mueller K.L., Cook B., Wu D., Zuker C.S., Ryba N.J.;
 RT "Coding of sweet, bitter, and umami tastes: different receptor cells sharing similar signaling pathways";
 RL Cell 112:293-301 (2003).
 RN [7]
 RP ACTIVATION BY SACHARIN AND ACESULFAME K.
 RX PubMed=15537898; DOI=10.1523/JNEUROSCI.1225-04.2004;
 RA Kuhn C., Bufo B., Winnig M., Hofmann T., Frank O., Behrens M., Lewtschenko T., Slack J.P., Ward C.D., Meyerhof W.;
 RT "Bitter taste receptors for saccharin and acesulfame K";
 RL J. Neurosci. 24:10260-10265 (2004).
 CC -!- FUNCTION: Receptor that may play a role in the perception of bitterness and is gustducin-linked. May play a role in sensing the chemical composition of the gastrointestinal content. The activity of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 activation and lead to the gating of TRPM5 (By similarity).
 CC Activated by the sulfonyl amide sweeteners saccharin and acesulfame K.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells

| | |
|---------------------------|--|
| CC | of the tongue and exclusively in gustducin-positive cells. |
| CC | -1- MISCELLANEOUS: Most taste cells may be activated by a limited |
| CC | number of bitter compounds; individual taste cells can |
| CC | discriminate among bitter stimuli. |
| CC | -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family. |
| CC | ----- |
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| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - |
| CC | the European Bioinformatics Institute. There are no restrictions on its |
| CC | use as long as its content is in no way modified and this statement is not |
| CC | removed. |
| CC | ----- |
| DR | ENBL; AF494228; AAM19319.1; -; Genomic DNA. |
| DR | ENBL; AY114090; AAM63540.1; -; Genomic DNA. |
| DR | ENBL; AY724942; AAU21144.1; -; Genomic DNA. |
| DR | Ensembl; ENSG0000183205; Homo sapiens. |
| DR | HCNC; HGNC:18881; TAS2R44. |
| DR | InterPro; IPR007960; TAS2_recept. |
| DR | PANTHER; PTHR11394; TAS2_2_recept; 1. |
| DR | Pfam; PF05296; TAS2R; 1. |
| KW | G-protein coupled receptor; Glycoprotein; Receptor; |
| KW | Sensory transduction; Taste; Transducer; Transmembrane. |
| FT | Extracellular (Potential). |
| FT | TOPO_DOM 1 2 |
| FT | TRANSEM 3 23 |
| FT | TOPO_DOM 24 55 |
| FT | TRANSEM 56 76 |
| FT | TOPO_DOM 77 100 |
| FT | TRANSEM 101 121 |
| FT | TOPO_DOM 122 126 |
| FT | TRANSEM 127 147 |
| FT | TOPO_DOM 148 181 |
| FT | TRANSEM 182 202 |
| FT | TOPO_DOM 203 229 |
| FT | TRANSEM 230 250 |
| FT | TOPO_DOM 251 259 |
| FT | TRANSEM 260 280 |
| FT | TOPO_DOM 281 309 |
| FT | CARBOHYD 161 161 |
| FT | CONFLICT 162 162 |
| FT | CONFLICT 227 227 |
| FT | CONFLICT 240 240 |
| FT | SEQUENCE 309 AA; 35296 MW; 56937C13952CB828 CRC64; |
| ST | ----- |
| Query Match | 89.4%; Score 1427; DB 1; Length 309; |
| Best Local Similarity | 89.6%; Pred.No. 1.3e-96; |
| Matches 277; Conservative | 12; Mismatches 20; Indels 0; Gaps 0; |
| QY | 1 MTFELPIFSSLVVTVFVIGNFANGFALVNSIERVKRKISADQILTALVSRVGLLW 60 |
| DB | : : : : : : : : : |
| QY | 1 MTFPIPIFSSVVVLFVIGNFANGFALVNSIERVKRKISADQILTALVSRVGLLW 60 |
| DB | : : : : : : : : : |
| QY | 61 VLLLNWYSTVLNPAFNSVEVRTTAYNIWAVINHFNSNWLATLSIFYLKIKAFNSFIPLH 120 |
| DB | : : : : : : : : : |
| QY | 61 VLLLNWYSTVFNPAFYSVEVRTTAYNWAVTGHFNSWLATLSIFYLKIKAFNSFIPLH 120 |
| DB | : : : : : : : : : |
| QY | 121 LKRVKSVILVMLGLPLFLACHLFFVINNMIEIVRTKEFEGNMTWKIKLSAMYSNNVT 180 |
| DB | : : : : : : : : : |
| QY | 121 LKRVKSVILVMLGLPLFLACQLFVINNMKEIVRTKEYEGNMTWKIKLSAVLSDATVT 180 |
| DB | : : : : : : : : : |
| QY | 181 MVANLVPTTLTLLSPMLLICSCLKHKKMQLHGKSGDSPSTKVHIKALQTVISFLLCAL 240 |
| DB | : : : : : : : : : |
| QY | 181 TLGNLVPTTLTLLCFLLLSLCSCLKHKKMQLHGKSGDSPSTKVHIKALQTVISFLLCAL 240 |
| DB | : : : : : : : : : |
| QY | 241 YFLSISIMSVSFGSLENKPVFMFCKAIRFSYPSIHPFILLWGNKKLQTFSLVFWQRYW 300 |
| DB | : : : : : : : : : |
| QY | 241 YFLSISIMSVSFGSLENKPVFMFCKAIRFSYPSIHPFILLWGNKKLQTFSLVLRQRYW 300 |
| DB | : : : : : : : : : |
| QY | 301 VKGEKTSPP 309 |
| DB | : : : : : : : : : |
| QY | 301 VKGEKTPSSP 309 |
| DB | : : : : : : : : : |

| | | | | | |
|-------|--|-----------------------------------|------|-----|-----|
| T2R46 | PANPA | STANDARD; | PRT; | 309 | AA. |
| ID | T2R46 | PANPA | | | |
| AC | Q646E1; | Q5Y4Z7; | | | |
| DT | 01-FEB-2005 | (Rel. 46, Created) | | | |
| DT | 01-FEB-2005 | (Rel. 46, Last sequence update) | | | |
| DT | 10-MAY-2005 | (Rel. 47, Last annotation update) | | | |
| DE | Taste receptor type 2 member 46 | (T2R46). | | | |
| GN | Name=TAS2R46; | | | | |
| OS | Pan paniscus (Pygmy chimpanzee) (Bonobo). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; | | | | |
| OC | Pan. | | | | |
| OX | NCBI_TaxID=9597; | | | | |
| RN | [1] | | | | |
| RN | NUCLEOTIDE SEQUENCE. | | | | |
| RP | PubMed=15496549; DOI=10.1093/molbev/msi027; | | | | |
| RX | Parry C.M., Erkner A., le Coutre J.; | | | | |
| RT | "Divergence of T2R chemosensory receptor families in humans, bonobos, | | | | |
| RT | and chimpanzees."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 101:14830-14834(2004). | | | | |
| CC | -1- FUNCTION: Receptor that may play a role in the perception of | | | | |
| CC | bitterness and is gustducin-linked. May play a role in sensing the | | | | |
| CC | chemical composition of the gastrointestinal content. The activity | | | | |
| CC | of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 | | | | |
| CC | activation and lead to the gating of TRPM5 (By similarity). | | | | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein. | | | | |
| CC | -1- MISCELLANEOUS: Most taste cells may be activated by a limited | | | | |
| CC | number of bitter compounds; individual taste cells can | | | | |
| CC | discriminate among bitter stimuli. | | | | |
| CC | -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family. | | | | |
| CC | ----- | | | | |
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| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - | | | | |
| CC | the European Bioinformatics Institute. There are no restrictions on its | | | | |
| CC | use as long as its content is in no way modified and this statement is not | | | | |
| CC | removed. | | | | |
| CC | ----- | | | | |
| DR | ENBL; AY724848; AAU21078.1; -; Genomic DNA. | | | | |
| DR | ENBL; AY677150; AAV28578.1; -; Genomic DNA. | | | | |
| DR | InterPro: IPR007960; TAS2_Recept. | | | | |
| DR | PANTHER; PTHR11394; TAS2_Recept; 1. | | | | |
| DR | Pfam; PF05236; TAS2R; 1. | | | | |
| KW | G-protein coupled receptor; Glycoprotein; Receptor; | | | | |
| KW | Sensory transduction; Taste; Transducer; Transmembrane. | | | | |
| FT | TOPO_DOM 1 1 | | | | |
| FT | TRANSMEM 2 22 | | | | |
| FT | TOPO_DOM 23 46 | | | | |
| FT | TRANSMEM 47 67 | | | | |
| FT | TOPO_DOM 68 86 | | | | |
| FT | TRANSMEM 87 107 | | | | |
| FT | TOPO_DOM 108 126 | | | | |
| FT | TRANSMEM 127 147 | | | | |
| FT | TOPO_DOM 148 178 | | | | |
| FT | TRANSMEM 179 199 | | | | |
| FT | TOPO_DOM 200 229 | | | | |
| FT | TRANSMEM 230 250 | | | | |
| FT | TOPO_DOM 251 259 | | | | |
| FT | TRANSMEM 260 280 | | | | |
| FT | TOPO_DOM 281 309 | | | | |
| FT | CARBOHYD 161 161 | | | | |
| FT | CARBOHYD 176 176 | | | | |
| FT | CONFLICT 177 177 | | | | |
| FT | CONFLICT 305 305 | | | | |
| FT | CONFLICT 309 309 | | | | |
| SQ | SEQUENCE 309 AA; 35644 MW; D1CF5966165C2B73 CRC64; | | | | |


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Best Local Similarity 87.4%; Pred. No. 1.3e-96;
Matches 270; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 1 MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLIW 60
FT TOPO DOM 24 55 Cytoplasmic (Potential).
FT TRANSMEM 56 76 2 (Potential).
FT TOPO DOM 77 100 Extracellular (Potential).
FT TRANSMEM 101 121 3 (Potential).
FT TOPO DOM 122 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT TOPO DOM 148 181 Extracellular (Potential).
FT TRANSMEM 182 202 5 (Potential).
FT TOPO DOM 203 229 Cytoplasmic (Potential).
FT TRANSMEM 230 259 6 (Potential).
FT TOPO DOM 251 280 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 309 AA; 35338 MW; 2B7C5152D4A36810 CRC64;

Query Match 88.9%; Score 1419; DB 1; Length 309;
Best Local Similarity 88.7%; Pred. No. 5.2e-96;
Matches 274; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 1 MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLIW 60
Db 1 MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLIW 60

QY 61 VLLNWSYTVLNPAPNSVEVETAYNIWAVINHFNSNLATLSIFYLKIANFSNFIPLH 120
Db 61 ALLNWSYTVENPAPNSVGVRTTVVDTVWTVGHFSNWLATSLSIFYLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLWMLGPLLFLACHLFLVNNNEIVRTKEEGNMTWKIKLSAMYSNMTVT 180
Db 121 LKRRVKSIVLWMLGPLLFLACHLFLVNNNEIVRTKEEGNMTWKIKLSAMYSNMTVT 180

QY 181 MVANLVPTTLTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
Db 181 TLANLVPTTLTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YFLSIMISVMSFGSLENKVPFMFCARFSPSIHPFILIWGNKKLQTFILSVFQMRYW 300
Db 241 YFLSIMISVMSFGSLENKVPFMFCARFSPSIHPFILIWGNKKLQTFILSVLRQVRYW 300

QY 301 VKGEKTSPP 309
Db 301 VKGEKPSSP 309

RESULT 14
T2R44 PONPY STANDARD; PRT; 309 AA.
ID T2R44 PONPY STANDARD; PRT; 309 AA.
AC Q645V3;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Taste receptor type 2 member 44 (T2R44).
GN Name=TAS2R44;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496549; DOI=10.1093/molbev/msi027;
RA Fischer A., Gilad Y., Man O., Paabo S.;
RT "Evolution of bitter taste receptors in humans and apes.";
CC Mol. Biol. Evol. 22:432-436(2005).
CC -!- FUNCTION: Receptor that may play a role in the perception of
CC bitterness and is gustducin-linked. May play a role in sensing the
CC chemical composition of the gastrointestinal content. The activity
CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC activation and lead to the gating of TRPM5 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
CC discriminate among bitter stimuli.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY724974; AAU21166.1; -; Genomic_DNA.
CC InterPro; IPR007960; TAS2_recept.
CC PANTHER; PTHR11394; TAS2_recept.
CC Pfam; PF05296; TAS2R; 1.
CC G-protein coupled receptor; Glycoprotein; Receptor;
CC Sensory transduction; Taste; Transducer; Transmembrane.
CC TOPO_DOM 1 2 Extracellular (Potential).
CC TRANSMEM 3 23 1 (Potential).
```

```
FT TOPO DOM 24 55 Cytoplasmic (Potential).
FT TRANSMEM 56 76 2 (Potential).
FT TOPO DOM 77 100 Extracellular (Potential).
FT TRANSMEM 101 121 3 (Potential).
FT TOPO DOM 122 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT TOPO DOM 148 181 Extracellular (Potential).
FT TRANSMEM 182 202 5 (Potential).
FT TOPO DOM 203 229 Cytoplasmic (Potential).
FT TRANSMEM 230 259 6 (Potential).
FT TOPO DOM 251 280 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT TOPO DOM 281 309 Cytoplasmic (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 309 AA; 35338 MW; 2B7C5152D4A36810 CRC64;

Query Match 88.9%; Score 1419; DB 1; Length 309;
Best Local Similarity 88.7%; Pred. No. 5.2e-96;
Matches 274; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 1 MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLIW 60
Db 1 MITFLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLIW 60

QY 61 VLLNWSYTVLNPAPNSVEVETAYNIWAVINHFNSNLATLSIFYLKIANFSNFIPLH 120
Db 61 ALLNWSYTVENPAPNSVGVRTTVVDTVWTVGHFSNWLATSLSIFYLKIANFSNFIPLH 120

QY 121 LKRRVKSIVLWMLGPLLFLACHLFLVNNNEIVRTKEEGNMTWKIKLSAMYSNMTVT 180
Db 121 LKRRVKSIVLWMLGPLLFLACHLFLVNNNEIVRTKEEGNMTWKIKLSAMYSNMTVT 180

QY 181 MVANLVPTTLTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
Db 181 TLANLVPTTLTLLSFMLLICSLCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240

QY 241 YFLSIMISVMSFGSLENKVPFMFCARFSPSIHPFILIWGNKKLQTFILSVFQMRYW 300
Db 241 YFLSIMISVMSFGSLENKVPFMFCARFSPSIHPFILIWGNKKLQTFILSVLRQVRYW 300

QY 301 VKGEKTSPP 309
Db 301 VKGEKPSSP 309

RESULT 14
T2R45 PANTR STANDARD; PRT; 309 AA.
ID T2R45 PANTR STANDARD; PRT; 309 AA.
AC Q646C0;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Taste receptor type 2 member 46 (T2R46).
GN Name=TAS2R46;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496549; DOI=10.1093/molbev/msi027;
RA Fischer A., Gilad Y., Man O., Paabo S.;
RT "Evolution of bitter taste receptors in humans and apes.";
CC Mol. Biol. Evol. 22:432-436(2005).
CC -!- FUNCTION: Receptor that may play a role in the perception of
CC bitterness and is gustducin-linked. May play a role in sensing the
CC chemical composition of the gastrointestinal content. The activity
CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC activation and lead to the gating of TRPM5 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
```

discriminate among bitter stimuli.
 -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.

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 EMBL; AY724877; AAU21099.1; -; Genomic_DNA.
 InterPro; IPR007960; TAS2_recept.
 Pfam; PF05296; TAS2R; 1.
 G-protein coupled receptor; Glycoprotein; Receptor;
 Sensory transduction; Taste; Transducer; Transmembrane.
 TOPO_DOM 1 1
 TRANSMEM 2 22
 TOPO_DOM 23 46
 TRANSMEM 47 67
 TOPO_DOM 68 86
 TRANSMEM 87 107
 TOPO_DOM 108 126
 TRANSMEM 127 147
 TOPO_DOM 148 178
 TRANSMEM 179 199
 TOPO_DOM 200 229
 TRANSMEM 230 259
 TOPO_DOM 260 280
 TRANSMEM 281 309
 CARBOHYD 161 161
 N-linked (GlcNAc...) (Potential).
 N-linked (GlcNAc...) (Potential).
 SEQUENCE 309 AA; 35603 MW; 0AB71A246FC89322 CRC64;

 Query Match 88.8%; Score 1418; DB 1; Length 309;
 Best Local Similarity 87.1%; Pred. No. 6.1e-96;
 Matches 269; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

 QY 1 MITPLPIFFSVLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
 DB 1 MITPLPIFFSVLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60

 QY 61 VLLNWSYTLNPAFNSVEVTTAYNWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120
 DB 61 VLLNWSYTLNPAFNSVEVTTAYNWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120

 QY 121 LKRRVKSIVLMLGPLLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
 DB 121 LKRRVKSIVLMLGPLLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

 QY 181 MVANLVPTLTLLSFMLLICSLCKHLKKWQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
 DB 181 ILANLVPTLTLLSFMLLICSLCKHLKKWQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240

 QY 241 YFLSIMISVWFSGLSENKPVFMFCARFSPSIHPFLLINGNKKLKQTFLLSVLHVRYW 300
 DB 301 VKGEKTSXP 309
 DB 301 VKGEKTSXP 309

 RESULT 15
 T2R46 GORGO
 ID T2R46 GORGO STANDARD; PRT; 309 AA.
 AC Q64527;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Taste receptor type 2 member 46 (T2R46).
 GN Name=TAS2R46;
 OS Gorilla gorilla gorilla (Lowland gorilla).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 Gorilla.
 NCBI_TaxID=9595;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496549; DOI=10.1093/molbev/msi027;
 RA Fischer A., Gilad Y., Man O., Paabo S.;
 RL "Evolution of bitter taste receptors in humans and apes."; Mol. Biol. Evol. 22:432-436(2005).
 CC -!- FUNCTION: Receptor that may play a role in the perception of bitterness and is gustducin-linked. May play a role in sensing the chemical composition of the gastrointestinal content. The activity of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 activation and lead to the gating of TRPM5 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited number of bitter compounds; individual taste cells can discriminate among bitter stimuli.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.

 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

 EMBL; AY724911; AAU21122.1; -; Genomic_DNA.
 InterPro; IPR007960; TAS2_recept.
 Pfam; PF05296; TAS2R; 1.
 G-protein coupled receptor; Glycoprotein; Receptor;
 Sensory transduction; Taste; Transducer; Transmembrane.
 TOPO_DOM 1 1
 TRANSMEM 2 22
 TOPO_DOM 23 46
 TRANSMEM 47 67
 TOPO_DOM 68 86
 TRANSMEM 87 107
 TOPO_DOM 108 126
 TRANSMEM 127 147
 TOPO_DOM 148 178
 TRANSMEM 179 199
 TOPO_DOM 200 229
 TRANSMEM 230 259
 TOPO_DOM 260 280
 TRANSMEM 281 309
 CARBOHYD 161 161
 N-linked (GlcNAc...) (Potential).
 SEQUENCE 309 AA; 35567 MW; 886893EDP27PF521 CRC64;

 Query Match 88.4%; Score 1412; DB 1; Length 309;
 Best Local Similarity 86.7%; Pred. No. 1.7e-95;
 Matches 267; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

 QY 1 MITPLPIFFSVLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
 DB 1 MITPLPIFFSVLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60

 QY 61 VLLNWSYTLNPAFNSVEVTTAYNWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120
 DB 61 VLLNWSYTLNPAFNSVEVTTAYNWAVINHFNSNWLATLSIFYLKIANFNSFIPLH 120

 QY 121 LKRRVKSIVLMLGPLLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
 DB 121 LKRRVKSIVLMLGPLLFLACHLFPVINNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180

 QY 181 MVANLVPTLTLLSFMLLICSLCKHLKKWQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
 DB 181 ILANLVPTLTLLSFMLLICSLCKHLKKWQLHGKSGQDPSTKVHIKALQTVISFLLCAI 240

 QY 241 YFLSIMISVWFSGLSENKPVFMFCARFSPSIHPFLLINGNKKLKQTFLLSVFQMRYW 300
 DB 241 YFLSIMISVWFSGLSENKPVFMFCARFSPSIHPFLLINGNKKLKQTFLLSVFQMRYW 300

Db 241 YFLSVIMSVSFBLSLENKPVFMFCEAITFSYPSTHPPFILWGNKCLKQTFLSVLWHVRYW 300
Qy 301 VKGEKTSS 308
|||
Db 301 VKGEKPSS 308

Search completed: April 27, 2006, 21:18:41
Job time : 167 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2006, 21:16:11 ; Search time 47 Seconds
(without alignments)
543.549 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MITFLPIIFSSLVVVFVIG.....FLSVFMQRYVWVGKTSPP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/PCUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 1115.5 | 69.8 | 300 | 2 | US-09-393-634-62 |
| 2 | 643 | 40.3 | 300 | 2 | US-09-393-634-58 |
| 3 | 614.5 | 38.5 | 317 | 2 | US-09-393-634-60 |
| 4 | 534.5 | 33.5 | 333 | 2 | US-09-393-634-3 |
| 5 | 534 | 33.4 | 318 | 2 | US-09-393-634-47 |
| 6 | 534 | 33.4 | 318 | 2 | US-09-949-016-9253 |
| 7 | 497.5 | 31.2 | 312 | 2 | US-09-393-634-51 |
| 8 | 480 | 30.1 | 144 | 2 | US-09-393-634-66 |
| 9 | 465 | 29.1 | 309 | 2 | US-09-393-634-49 |
| 10 | 463 | 29.0 | 307 | 2 | US-09-393-634-53 |
| 11 | 459 | 28.7 | 129 | 2 | US-09-393-634-72 |
| 12 | 459 | 28.7 | 300 | 2 | US-09-393-634-19 |
| 13 | 448 | 28.1 | 300 | 2 | US-09-393-634-17 |
| 14 | 440.5 | 27.6 | 316 | 2 | US-09-393-634-39 |
| 15 | 440.5 | 27.6 | 316 | 2 | US-09-949-016-8207 |
| 16 | 429 | 26.9 | 121 | 2 | US-09-393-634-70 |
| 17 | 426.5 | 26.7 | 310 | 2 | US-09-393-634-7 |
| 18 | 417.5 | 26.1 | 315 | 2 | US-09-393-634-56 |
| 19 | 395.5 | 24.8 | 266 | 2 | US-09-393-634-15 |
| 20 | 333.5 | 20.9 | 180 | 2 | US-09-393-634-33 |
| 21 | 326 | 20.4 | 299 | 2 | US-09-393-634-35 |
| 22 | 320.5 | 20.1 | 299 | 2 | US-09-393-634-43 |
| 23 | 320.5 | 20.1 | 299 | 2 | US-09-949-016-6942 |
| 24 | 320.5 | 20.1 | 299 | 2 | US-09-949-016-8156 |
| 25 | 314.5 | 19.7 | 302 | 2 | US-09-393-634-37 |
| 26 | 305 | 19.1 | 224 | 2 | US-09-393-634-9 |
| 27 | 297 | 18.6 | 335 | 2 | US-09-393-634-1 |

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|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 284 | 17.8 | 209 | 2 | US-09-393-634-13 | Sequence 13, Appl |
| 29 | 276.5 | 17.3 | 299 | 2 | US-09-393-634-41 | Sequence 41, Appl |
| 30 | 271.5 | 17.0 | 299 | 2 | US-09-393-634-5 | Sequence 5, Appl |
| 31 | 263 | 16.5 | 291 | 2 | US-09-949-016-8213 | Sequence 8213, Ap |
| 32 | 255 | 16.0 | 65 | 2 | US-09-393-634-74 | Sequence 74, Appl |
| 33 | 255 | 16.0 | 291 | 2 | US-09-393-634-64 | Sequence 64, Appl |
| 34 | 255 | 16.0 | 291 | 2 | US-09-949-016-6919 | Sequence 6919, Ap |
| 35 | 248 | 15.5 | 173 | 2 | US-09-393-634-23 | Sequence 23, Appl |
| 36 | 228 | 14.3 | 155 | 2 | US-09-393-634-21 | Sequence 21, Appl |
| 37 | 198 | 12.4 | 115 | 2 | US-09-393-634-27 | Sequence 27, Appl |
| 38 | 196 | 12.3 | 245 | 2 | US-09-393-634-55 | Sequence 55, Appl |
| 39 | 180 | 11.3 | 167 | 2 | US-09-949-016-8853 | Sequence 8853, Ap |
| 40 | 177 | 11.1 | 126 | 2 | US-09-393-634-31 | Sequence 31, Appl |
| 41 | 151.5 | 9.5 | 68 | 2 | US-09-393-634-29 | Sequence 29, Appl |
| 42 | 143 | 9.0 | 72 | 2 | US-09-393-634-78 | Sequence 78, Appl |
| 43 | 137 | 8.6 | 87 | 2 | US-09-393-634-68 | Sequence 68, Appl |
| 44 | 130.5 | 8.2 | 380 | 1 | US-08-153-848-40 | Sequence 40, Appl |
| 45 | 130.5 | 8.2 | 380 | 2 | US-09-299-843A-40 | Sequence 40, Appl |

ALIGNMENTS

RESULT 1
US-09-393-634-62
; Sequence 62, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 023078-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR15
; NAME/KEY: MOD RES
; LOCATION: (257)
; OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-62

Query Match 69.8%; Score 1115.5; DB 2; Length 300;
Best Local Similarity 72.2%; Pred. No. 1.4e-105;
Matches 216; Conservative 34; Mismatches 48; Indels 1; Gaps 1;

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| Qy | 1 | MITFLPIIFSSLVVVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW | 60 |
| Db | 1 | MITFLPIIFSSLVVVFVIGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW | 60 |
| Qy | 61 | VLLLNWSTVLNPAFNSVEVTTAYNIWAVLNHFSNMLATLISFYLLKIANFSNFIPLH | 120 |
| Db | 61 | VILLHWATVLPNGSYSLGVATTINAWAVNHFSIWATSLISFYFLKIANFSNFIPLH | 120 |
| Qy | 121 | LKRVKSVILVMLGLPLFLACHLFPVNNMNIIVTKPEGNMTWKIKLSAMYFSNMTVT | 180 |
| Db | 121 | LKRIKSVIPVILLGSLFLVCHLVVNMDSMTWKKEYEGNVSWEIKLSDPHTLSDMTMT | 180 |
| Qy | 181 | MVANIIVPPTLLISFMILLICSLCKHLKMKQHLGKSGDPSTKVKHTKALQTVISFLLCAI | 240 |
| Db | 181 | TLANLIPPTLSLLSFLLLCKHLKMKQPHGKSGDPSTKVKHTKALQTVISFLLFAV | 240 |

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QY 241 YELSIMISWSP-GSLENKPVFMFCKAIRFSYPSIHPFILLGNKKLQKOTFLSVFQWR 298
Db 241 YFLSLITSWNRRRLXNEPVLMLSQTTAIYPSFHSFILLWGSKGLKQTFLLILCQIK 299

RESULT 2
US-09-393-634-58
; Sequence 58, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR13
US-09-393-634-58

Query Match 40.3%; Score 643; DB 2; Length 300;
Best Local Similarity 46.3%; Pred. No. 2.2e-57;
Matches 139; Conservative 54; Mismatches 95; Indels 12; Gaps 5;

QY 1 MITPLPIFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
Db 1 MESALPISFTLVIIAEFIIGNLSNGFIVLNCIDWVSKRELSSVDKLLIILAISRIGLIW 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTAYNI----WAVINHSNMLATLSIFYLKIANFNGF 116
Db 61 ELVSWP---LALHVLAFVSTGURIMTFSVINSHFNMLATIFSIFYLKIASFSP 117

QY 117 IFLHLKRRVKSIVLWMLGPLLFLACHLFINNNEIVRTKEPEGNMTWKIKLSAMYFS- 175
Db 118 APLYLKRWNVKIVMLLGLTFLVFLNLTIQNNHIKMDLDRYERTTNWFSMSDFETFSV 177

QY 176 --NMTVTWVANLVPETLLSFMLLICSCLKHKKMLHKGSDPSTKVHILKALQTVIS 233
Db 178 SVKFTWMP-SUTPTFVAFISFLLIFSLQKHLQKMLNYKGRDRPTKVTNALKIVIS 236

QY 234 FLLLCALYFLSIMSWSGSLENKPVFMFCKAIRFSYPSIHPFILLGNKKLQKOTFLSV 293
Db 237 FLLFASFLCLVLIS-WISELQNTVIYMLCETIGVPSPSHSLFLLILGNKLRQAFLV 295

RESULT 3
US-09-393-634-60
; Sequence 60, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
```

```
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR14
US-09-393-634-60

Query Match 38.5%; Score 614.5; DB 2; Length 317;
Best Local Similarity 46.2%; Pred. No. 1.9e-54;
Matches 140; Conservative 52; Mismatches 106; Indels 5; Gaps 4;

QY 8 IFSSLVVTVFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLWLLNMY 67
Db 8 IFTFVLIVFIFIGNLSNGFIALVNCIDWVKGKISSVDRILTLAISRLWLFSGWC 67

QY 68 STVLNPA-FNSVEVRTAYNIWAVINHSNMLATLSIFYLKIANFNFIFLHLKRRVK 126
Db 68 VSVFPFALFATEKMPRLTNITWVINFHSVWLATGLGTFYFLKIANFNSIEFLYLKRWVK 127

QY 127 SVILWMLGPLLFLACHLFINNNEIVRTKEPEGNMTWKIKLSAMYFSNMTV--TMVAN 184
Db 128 KVLVLLLVTVFVFLPFLNIALININASINGYRRNKTCSDDSNFTRESSLIVLTSTVPI 187

QY 185 LVPFTLLSFMLLICSCLKHKKMLHKGSDPSTKVHILKALQTVISFLLLCALYFLS 244
Db 188 FIPFTLSLAMEFLLIFSNWKKRKKQHTVKISGDASTKAH-RGVKSVITFFLLYAFSL 246

QY 245 IMISWSGSLENKPVFMFCKAIRFSYPSIHPFILLGNKKLQKOTFLSVFQWRVYVKG 304
Db 247 FFISVMTSERLEEN-LIILSQVMGMAYPSCHSVLILGNKKLRQASLSVLLWLRVYMKDG 305

QY 305 KTS 307
Db 306 EPS 308

RESULT 4
US-09-393-634-3
; Sequence 3, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat GR02
US-09-393-634-3

Query Match 33.5%; Score 534.5; DB 2; Length 333;
Best Local Similarity 41.4%; Pred. No. 3e-46;
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Matches 126; Conservative 52; Mismatches 107; Indels 19; Gaps 4;

Qy 9 FSSLVVTVFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLWVLLWVYS 68
 Db 14 FSIIFYVEIVTGILNGFIALVNDWLKRRISTADQILTALATRLIYVWSVLICILL 73

Qy 69 TVLWPAFN-SVEVTTAYNIWAVINHFNSWLTATLSIFYLKIANFNSFIFLHLKRRVKS 127
 Db 74 LFLCPHLSMRPEMFTAIGVIVVDNHFISWLTATLCLGVFYLKIASFNSLFLYLKRWYK 133

Qy 128 VILVMLGLPLFLACHLFLVNNNEIVRTKEPEGNNMTKI-----KLKSAMYFSNMT-VMV 182
 Db 134 VLMILILSLFLMLNISGLMYHFSIDVTGNNMSYLVNDSTHPRPLFTNSKVFLLI 193

Qy 183 AN-----LVFTTLTSLFMLLISCLCKHKLKQMLHGKSGQDPSTKVHIKALQ 229
 Db 194 ANSSHVPPLNSLFLMIFFTVSLVAFFVFLSLWKHKHKKQVNAKGRPRDASTMAHTKALQ 253

Qy 230 TVISFLLCAIYFLSIMSVSFGSLKNPKVPMFCKATRFSPYSIHPFILLWGNKKLQOT 289
 Db 254 IGFSEFLLYAIYLLFIITGILNLDLMRCIVILLFDHISGAVFSISHSFVLILGNSKLQRA 313

Qy 290 FLSV 293
 Db 314 TLSV 317

RESULT 5
 US-09-393-634-47
 ; Sequence 47, Application US/09393634
 ; Patent No. 6558910
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Adler, Jon Elliot
 ; APPLICANT: Ryba, Nick
 ; APPLICANT: Mueller, Ken
 ; APPLICANT: Hoon, Mark
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
 ; FILE REFERENCE: 02307E-098000US
 ; CURRENT APPLICATION NUMBER: US/09/393,634
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human GR07
 US-09-393-634-47

Query Match 33.4%; Score 534; DB 2; Length 318;
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 Matches 122; Conservative 58; Mismatches 109; Indels 16; Gaps 6;

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 Db 12 LAVGEFSVGLIGNAFIGLVNCDWYKVKKIASIDILTSLAISRCLLCVILLDCFILVL 71

Qy 72 NPAFNSV--EVRTTAYNIWAVINHFNSWLTATLSIFYLKIANFNSFIFLHLKRRVKSVI 129
 Db 72 YPDVYATGKEMRIIDP-FWLTNLHLSIWFACTLSIYFFKIGNFPHFLPFWKWKRIDRVI 130

Qy 130 LVMLLGPLLFLACHLFLVI-----NNNE-----IVRTKEPEGNNMTWKIKLSAMYFSNMTVT 180
 Db 131 SWILLCVVL---SVFISLPATENLNADRFVCVAKR-KTNLTWSCRVNKTQHASTKFLFL 186

Qy 181 MVANLVPTLTLSPMLLISCLCKHKLKQMLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
 Db 187 NLATLLPFCVCLMSFFLLILSLRRHRRMQUSATGCRDPSTEAHVRAKAVISFLLFLTA 246

Qy 241 YFLSIMISVMSFGSLENKPVFMFCKATRFSPYSIHPFILLWGNKKLQOTFISVFMQRYW 300
 Db 247 YLFLATLTSYFMPETELAVIFGESIALIYPSSHSFILILGNNKLRHASLKVIVKWSI 306

Qy 301 VKGEK 305
 Db 307 LKGRK 311

RESULT 7
 US-09-393-634-51
 ; Sequence 51, Application US/09393634
 ; Patent No. 6558910
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Adler, Jon Elliot
 ; APPLICANT: Ryba, Nick

Db 187 NLATLLPFCVCLMSFFLLILSLRRHRRMQUSATGCRDPSTEAHVRAKAVISFLLFLTA 246

Qy 241 YFLSIMISVMSFGSLENKPVFMFCKATRFSPYSIHPFILLWGNKKLQOTFISVFMQRYW 300
 Db 247 YLFLATLTSYFMPETELAVIFGESIALIYPSSHSFILILGNNKLRHASLKVIVKWSI 306

Qy 301 VKGEK 305
 Db 307 LKGRK 311

RESULT 6
 US-09-949-016-9253
 ; Sequence 9253, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9253
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-9253

Query Match 33.4%; Score 534; DB 2; Length 318;
 Best Local Similarity 40.0%; Pred. No. 3.2e-46;
 Matches 122; Conservative 58; Mismatches 109; Indels 16; Gaps 6;

Qy 12 LVVTVFVIGNFANGFIALVNSIEWFKROKISFADQILTALAVSRVGLLWVLLWVYSVL 71
 Db 12 LAVGEFSVGLIGNAFIGLVNCDWYKVKKIASIDILTSLAISRCLLCVILLDCFILVL 71

Qy 72 NPAFNSV--EVRTTAYNIWAVINHFNSWLTATLSIFYLKIANFNSFIFLHLKRRVKSVI 129
 Db 72 YPDVYATGKEMRIIDP-FWLTNLHLSIWFACTLSIYFFKIGNFPHFLPFWKWKRIDRVI 130

Qy 130 LVMLLGPLLFLACHLFLVI-----NNNE-----IVRTKEPEGNNMTWKIKLSAMYFSNMTVT 180
 Db 131 SWILLCVVL---SVFISLPATENLNADRFVCVAKR-KTNLTWSCRVNKTQHASTKFLFL 186

Qy 181 MVANLVPTLTLSPMLLISCLCKHKLKQMLHGKSGQDPSTKVHIKALQTVISFLLCAI 240
 Db 187 NLATLLPFCVCLMSFFLLILSLRRHRRMQUSATGCRDPSTEAHVRAKAVISFLLFLTA 246

Qy 241 YFLSIMISVMSFGSLENKPVFMFCKATRFSPYSIHPFILLWGNKKLQOTFISVFMQRYW 300
 Db 247 YLFLATLTSYFMPETELAVIFGESIALIYPSSHSFILILGNNKLRHASLKVIVKWSI 306

Qy 301 VKGEK 305
 Db 307 LKGRK 311

RESULT 7
 US-09-393-634-51
 ; Sequence 51, Application US/09393634
 ; Patent No. 6558910
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Adler, Jon Elliot
 ; APPLICANT: Ryba, Nick

```
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 312
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR09
US-09-393-634-51

Query Match      31.2%; Score 497.5; DB 2; Length 312;
Best Local Similarity 36.6%; Pred. No. 1.6e-42;
Matches 118; Conservative 59; Mismatches 122; Indels 23; Gaps 5;

QY 1 MITELPIFSSLVVTVFVGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLW 60
Db 1 MPEAEAYIIILAGELTIGWNGFVVLVNCIDMLKRDLSLIDIIILSLAISRICLLC 60

QY 61 VLLLNWYSTVLNPAFNSVEVRTAYN-IWAVINHFSNMLATLSIFYLKIANFSNFIFL 119
Db 61 VISLDGFFMLLPFGTYGNSVLVSIVNVWTPANNSSLWFTSCLSIFYLKIANISHPFPF 120

QY 120 HLKRRVKSIVLMLGLPLF-----LACHLFVNMMIEIVRTKEFEGNWTWKIL 168
Db 121 WLKLIKINKYMLAIIIGSLFISLIISVPKNDMMYHLFKVSHBE-----NITWPKFV 171

QY 169 -KSAMVFSNMVTVMANLVPFTLLSFMLLICSLCKHLKQWLHGKSGODPSTKVHIKA 227
Db 172 SKIPGTFKQLTUNL-GVWVPFLCHISFLLFLSLVHTKQIRLHATGRDSTAHWRA 230

QY 228 LQTIVISFLLLCIAIFLSIMSVMSFGSLENKPFVFMCKAIRFSYPSIHPFILWGNKKLK 287
Db 231 IKAVIIFLLLLIVYVPVFLVMTSSALIPOGLVLMIGDIVTVTFPSSHFILMGNSKL 290

QY 288 QTFSLVFWQRYWVKGKTSPP 309
Db 291 EAFKMLRFVKCFLLRRKPFVP 312
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RESULT 8
US-09-393-634-66
; Sequence 66, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 144
; TYPE: PR1
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: human GR17
; NAME/KEY: MOD_RES
; LOCATION: (54)
; OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-66

Query Match      30.1%; Score 480; DB 2; Length 144;
Best Local Similarity 66.9%; Pred. No. 3.6e-41;
Matches 95; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 8 IFSSLVVTVFVGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLWLLWY 67
Db 2 ILSILVFAVLGNVANGFIALVNVNDWVKTKSSSTQIVTALAFSRLGLLXILLHWY 61

QY 68 STVLNPAFNSVEVRTAYNIWAVINHFSNMLATLSIFYLKIANFSNFIFLHLKRRVKS 127
Db 62 ATVFNSALYSLEVRIVPSNVSAIINHFSIWLATLSIFYLKIANFSNFIFLHLKRIKS 121

QY 128 VILVMLGLPLFLACHLFVINM 149
Db 122 VLLVILLGSLVFLICNLAVTM 143

RESULT 9
US-09-393-634-49
; Sequence 49, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 309
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR08
US-09-393-634-49

Query Match      29.1%; Score 465; DB 2; Length 309;
Best Local Similarity 35.2%; Pred. No. 3.3e-39;
Matches 103; Conservative 69; Mismatches 109; Indels 12; Gaps 3;

QY 8 IFSSLVVTVFVGNFANGFIALVNSIEWFKQKISFADQIILTALAVSRVGLLWLLWY 67
Db 8 IFILITGEFTIGLNGYIALVNVNDWIKKKISTVDYILTNLVIARICLISVMVNGI 67

QY 68 STVLNPAFNSVEVRTAYNIWAVINHFSNMLATLSIFYLKIANFSNFIFLHLKRRVKS 126
Db 68 VIVLNPVYTKNQIIVFTFTFANYLNMMITCLNVFYFLKIASSSHPLFLWKWKID 127

QY 127 SVILVMLGLPLFLACHLFVINMNEIVRTKEF-----EGNWTWKILKSAMVFSNM 178
Db 128 MVVHWILIG--CFALISLLVSLIAIVLSVCDYRFRHAIARHKNITEMFHVSKIPFEPL 184

QY 179 VTMVANLVPFTLLSFMLLICSLCKHLKQWLHGKSGODPSTKVHIKALQTVISFLLLC 238
Db 185 LFNLFAPVFFVLSLISFLLVRLSRHRTKQIKLYATGSRDPESTEVHVAIKNTWTFIFPF 244

QY 239 AIYFLSIMSVMSFGSLENKPFVFMCKAIRFSYPSIHPFILWGNKKLKQTF 291
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Db 68 AKLFYPSKYFSSLSLEIISY-IMTVNHLTWFAISLSIFVFLKIANFSDCVFLWKERT 126
QY 126 KSVILVMLLGPLL--FLACHLFI-----NNNEIVRTKEPEGNTWKIKLSAMY-PSN 176
Db 127 DKA-FVFLGCLLTSWISFVSFVVMKDGKVNHRNTSE-----MYWEKROFTINYVFLN 181
QY 177 MTTVMVANLVPFTLLSFMLLICSLCKHLKQMLHKGSDPSTKVHIKALQTVISPLL 236
Db 182 IGVISL-----FMWTLTACFLIMSLWRHSRQMSGVSGFRDLNTEAHVKAIFLISFI 236
QY 237 LCIAIFLSIMISVMSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQ 296
Db 237 LFVLYFIGVIBIICIFIPENKLLIFIGFTTASIYPCCHSFILLIISNQLKQAFVKVLOQ 296
QY 297 MRYW 300
Db 297 LKFF 300
RESULT 13
US-09-393-634-17
; Sequence 17, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; NUMBER OF SEQ ID NOS: 92
; CURRENT FILING DATE: 1999-09-10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse GR04
US-09-393-634-17

Query Match 28.1%; Score 448; DB 2; Length 300;
Best Local Similarity 33.3%; Pred. No. 1.7e-37;
Matches 101; Conservative 66; Mismatches 126; Indels 10; Gaps 3;
QY 1 MITPLPIIPSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLW 60
Db 1 MLSALESILLSVATSEAMGLVGLNTFIVLVNYTDVNRNKLKSKINFILTLAISRIFTW 60
QY 61 VLLLNWYS-----TVLNPAFNSVEVRTTAYNINWVNFHPSNWLATLSIFYLLKIANFSN 115
Db 61 IITLDAYTKVFLTLWMPES-----SLHECMSYIWIINHLVSWFSTLSGIFVFLKIANFSH 116
QY 116 FIFLHKKRVKSVILVMLLGPLLFLACHLFLVNMMNEIVRTKEFEGNTWKIKLSAMYFS 175
Db 117 YIFLWKKRADKV-FVFLIVFLLIITWLASFPLAVKIKDVKIYQNTSWLHLESELLI 175
QY 176 NMTVTVANLVPFTLLSFMLLICSLCKHLKQMLHKGSDPSTKVHIKALQTVISPL 235
Db 176 NYVFANMGPISLFIIVAIACFLITISLWRHSRQMSIGSGFRDLNTEAHMKAMKVLIAFI 235
QY 236 LCIAIFLSIMISVMSFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFW 295
Db 236 ILFIFYLGILITETLCLEFTNNKLLIFIGFTTUSAMYPCCHSFILITLSRELKQDTMRALQ 295
QY 296 QMR 298

Db 296 RLK 298
RESULT 14
US-09-393-634-39
; Sequence 39, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; NUMBER OF SEQ ID NOS: 92
; CURRENT FILING DATE: 1999-09-10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR03
US-09-393-634-39
Query Match 27.6%; Score 440.5; DB 2; Length 316;
Best Local Similarity 37.0%; Pred. No. 1.1e-36;
Matches 108; Conservative 56; Mismatches 117; Indels 11; Gaps 5;
QY 8 IFSSLVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLWVLLNMY 67
Db 8 VFLILSGTQFTLIGILVNCFIELVNGSSWFKTRMSLSDFIITLALLAILLCILITDSF 67
QY 68 STVLNPAFNSVEVRTTAYNI-WAVINHPNSNWLATLSIFYLLKIANFSNFIPLHLKRRVK 126
Db 68 LIEFSPNTHDSGIIMQIIDVSWTFNHLISWLATCLGVLYCLKIASFSGHPTPLMKRVS 127
QY 127 SVILVMLLGPLLFLACHLFLVNMMNEIVRTKEFEG-----NMTWKIKLSAMYFSNWTVM 181
Db 128 RVWVWMLLALL-LSCGSTASLINEFELKLYSVRGIEATRNVTETPKRSEYLLIHLVLT 186
QY 182 VANLVPFTLLSFMLLICSLCKHLKQMLHKGSDPSTKVHIKALQTVISFLLLCIAY 241
Db 187 LWYLPPLIVSLASVLLIFSLGRHTRQMLONGTSRDRPTTEAKRAIRIILSFFFLFLY 246
QY 242 FLSIMISVMSFGSL--ENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTF 291
Db 247 FLAPLIA--SFGNPLPKTKMAKMGIVMTFYPAGHSFILIGNSKLKQTFV 296
RESULT 15
US-09-949-016-8207
; Sequence 8207, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:18:56 ; Search time 121 Seconds
(without alignments)
1067.019 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MITFLPIFSSLVVTVFVIG.....FLSVFQMRVVKGTSSP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.psp:
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.psp:
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.psp:
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.psp:
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.psp:
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.psp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------------|
| 1 | 1597 | 100.0 | 309 | 3 | US-09-825-882-8 |
| 2 | 1597 | 100.0 | 309 | 4 | US-10-017-161-1836 |
| 3 | 1597 | 100.0 | 309 | 4 | US-10-191-058-5 |
| 4 | 1597 | 100.0 | 309 | 4 | US-10-292-798-1492 |
| 5 | 1597 | 100.0 | 309 | 4 | US-10-343-650A-682 |
| 6 | 1597 | 100.0 | 309 | 4 | US-10-724-208-8 |
| 7 | 1597 | 100.0 | 309 | 4 | US-10-770-127-179 |
| 8 | 1597 | 100.0 | 309 | 5 | US-10-724-209-8 |
| 9 | 1597 | 100.0 | 309 | 5 | US-10-986-871-8 |
| 10 | 1440 | 90.2 | 309 | 3 | US-09-825-882-20 |
| 11 | 1440 | 90.2 | 309 | 4 | US-10-017-161-1932 |
| 12 | 1440 | 90.2 | 309 | 4 | US-10-292-798-1584 |
| 13 | 1440 | 90.2 | 309 | 4 | US-10-724-208-20 |
| 14 | 1440 | 90.2 | 309 | 5 | US-10-724-209-20 |
| 15 | 1440 | 90.2 | 309 | 5 | US-10-986-871-20 |
| 16 | 1438 | 90.0 | 309 | 4 | US-10-770-127-191 |
| 17 | 1424 | 89.2 | 309 | 3 | US-09-825-882-12 |
| 18 | 1424 | 89.2 | 309 | 4 | US-10-219-834-18 |
| 19 | 1424 | 89.2 | 309 | 4 | US-10-017-161-1838 |
| 20 | 1424 | 89.2 | 309 | 4 | US-10-292-798-1494 |
| 21 | 1424 | 89.2 | 309 | 4 | US-10-343-650A-692 |
| 22 | 1424 | 89.2 | 309 | 4 | US-10-724-208-12 |
| 23 | 1424 | 89.2 | 309 | 4 | US-10-724-207-183 |
| 24 | 1424 | 89.2 | 309 | 5 | US-10-724-209-12 |
| 25 | 1424 | 89.2 | 309 | 5 | US-10-986-871-12 |
| 26 | 1348 | 84.4 | 299 | 3 | US-09-510-332-76 |
| 27 | 1348 | 84.4 | 299 | 4 | US-10-292-798-1480, Ap |

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|----|------|------|-----|---|--------------------|-------------------|
| 28 | 1348 | 84.4 | 299 | 4 | US-10-343-650A-670 | Sequence 670, Ap |
| 29 | 1348 | 84.4 | 299 | 4 | US-10-770-127-76 | Sequence 76, Ap |
| 30 | 1348 | 84.4 | 299 | 5 | US-10-962-365-76 | Sequence 76, Ap |
| 31 | 1334 | 83.5 | 298 | 4 | US-10-017-161-1824 | Sequence 1824, Ap |
| 32 | 1299 | 81.3 | 319 | 4 | US-10-017-161-1826 | Sequence 1826, Ap |
| 33 | 1299 | 81.3 | 319 | 4 | US-10-292-798-1482 | Sequence 1482, Ap |
| 34 | 1293 | 81.0 | 319 | 3 | US-09-510-332-70 | Sequence 3, Ap |
| 35 | 1293 | 81.0 | 319 | 4 | US-10-191-058-3 | Sequence 668, Ap |
| 36 | 1293 | 81.0 | 319 | 4 | US-10-343-650A-668 | Sequence 70, Ap |
| 37 | 1293 | 81.0 | 319 | 4 | US-10-770-127-70 | Sequence 70, Ap |
| 38 | 1293 | 81.0 | 319 | 5 | US-10-962-365-70 | Sequence 70, Ap |
| 39 | 1285 | 80.5 | 309 | 3 | US-09-510-332-56 | Sequence 56, Ap |
| 40 | 1285 | 80.5 | 309 | 5 | US-10-962-365-56 | Sequence 56, Ap |
| 41 | 1273 | 79.7 | 309 | 4 | US-10-770-127-56 | Sequence 56, Ap |
| 42 | 1215 | 76.1 | 299 | 3 | US-09-510-332-53 | Sequence 53, Ap |
| 43 | 1215 | 76.1 | 299 | 4 | US-10-770-127-53 | Sequence 53, Ap |
| 44 | 1215 | 76.1 | 299 | 5 | US-10-962-365-53 | Sequence 53, Ap |
| 45 | 1185 | 74.2 | 319 | 3 | US-09-510-332-51 | Sequence 51, Ap |

ALIGNMENTS

RESULT 1

US-09-825-882-8
; Sequence 8, Application US/09825882
; Patent No. US20020094551A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/09/825,882
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-825-882-8

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|-----------------------|---------|---|-----------|------------|----|--------|------|
| Query Match | 100.0%; | Score | 1597; | DB | 3; | Length | 309; |
| Best Local Similarity | 100.0%; | Pred. No. | 5.9e-139; | | | | |
| Matches | 309; | Conservative | 0; | Mismatches | 0; | Indels | 0; |
| Gaps | 0; | | | | | | |
| Qy | 1 | MITFLPIFSSLVVTVFVIGNFANGFTALVNSIEWFKROKISPADQILTALAVSRVGLLW | 60 | | | | |
| Db | 1 | MITFLPIFSSLVVTVFVIGNFANGFTALVNSIEWFKROKISPADQILTALAVSRVGLLW | 60 | | | | |
| Qy | 61 | VLLNWTSTVLNPAFNSVEVTRTAYNIWAVNHNPSNMLATLTSIFYLKIANFSNFIPLH | 120 | | | | |
| Db | 61 | VLLNWTSTVLNPAFNSVEVTRTAYNIWAVNHNPSNMLATLTSIFYLKIANFSNFIPLH | 120 | | | | |
| Qy | 121 | LKRRVKSIVLLMGLPFLFLACHLFINNMEIVRTKEFGNMTWKIKLSAMYSFNTVT | 180 | | | | |
| Db | 121 | LKRRVKSIVLLMGLPFLFLACHLFINNMEIVRTKEFGNMTWKIKLSAMYSFNTVT | 180 | | | | |
| Qy | 181 | MVANLVPFTLLSFMILLISLCKHLKQNLHGKSGDPSPTKVHKALQTVISFLLCAI | 240 | | | | |
| Db | 181 | MVANLVPFTLLSFMILLISLCKHLKQNLHGKSGDPSPTKVHKALQTVISFLLCAI | 240 | | | | |
| Qy | 241 | YFLSIMISVMSFSGLENKPVFMFCKAIRFSVPSIHPFILWGNKKLQOTPLSVFWMQRYW | 300 | | | | |
| Db | 241 | YFLSIMISVMSFSGLENKPVFMFCKAIRFSVPSIHPFILWGNKKLQOTPLSVFWMQRYW | 300 | | | | |
| Qy | 301 | VKGEKTSPP 309 | | | | | |
| Db | 301 | VKGEKTSPP 309 | | | | | |

RESULT 2
US-10-161-1836
; Sequence 1836, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1836
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-1836

Query Match 100.0%; Score 1597; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.9e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
DB 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
QY 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEPEGNTWKIKLKSAMYFSNMTVT 180
DB 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEPEGNTWKIKLKSAMYFSNMTVT 180
QY 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240
DB 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240
QY 241 YFLSTMISVWFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMRYW 300
DB 241 YFLSTMISVWFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309

RESULT 3
US-10-191-058-5
; Sequence 5, Application US/10191058
; Publication No. US20030170608A1
; GENERAL INFORMATION:
; APPLICANT: PRONIN, ALEXEY
; APPLICANT: CONNOR, JUDY
; APPLICANT: TANG, HUIXIAN
; APPLICANT: KEUNG, WALTER
; APPLICANT: SERVANT, GUY
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: BRUST, PAUL
; TITLE OF INVENTION: USE OF SPECIFIC T2R TASTE RECEPTORS TO IDENTIFY
; FILE REFERENCE: 078003-0280784
; CURRENT APPLICATION NUMBER: US/10/191,058
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/303,811
; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/372,089
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-191-058-5

Query Match 100.0%; Score 1597; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.9e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
DB 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
QY 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEPEGNTWKIKLKSAMYFSNMTVT 180
DB 121 LKRRVKSVILVMLGPLLFLACHLFPVINNMNEIVRTKEPEGNTWKIKLKSAMYFSNMTVT 180
QY 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240
DB 181 MVANLVPTTLTLLSPMLLICSCKHLKXQQLHGKSGQDPSTKVHIKALQTVISFLLLCAL 240
QY 241 YFLSTMISVWFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMRYW 300
DB 241 YFLSTMISVWFGSLENKPVFMFCKAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMRYW 300
QY 301 VKGEKTSPP 309
DB 301 VKGEKTSPP 309

RESULT 4
US-10-292-798-1492
; Sequence 1492, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1492
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-1492

Query Match 100.0%; Score 1597; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.9e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
DB 1 MITPLPIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
QY 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
DB 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120

Db 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
Qy 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Qy 181 MVANLVPPTLLTLLSFMLLICSCLKHLKKQQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240
Db 181 MVANLVPPTLLTLLSFMLLICSCLKHLKKQQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240
Qy 241 YFLSMTISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFQWQRYW 300
Db 241 YFLSMTISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFQWQRYW 300
Qy 301 VKGEKTSSP 309
Db 301 VKGEKTSSP 309

RESULT 5

US-10-343-650A-682
; Sequence 682, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 682
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-682

Query Match 100.0%; Score 1597; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.9e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
Db 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
Qy 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
Db 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
Qy 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Qy 181 MVANLVPPTLLTLLSFMLLICSCLKHLKKQQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240
Db 181 MVANLVPPTLLTLLSFMLLICSCLKHLKKQQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240
Qy 241 YFLSMTISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFQWQRYW 300
Db 241 YFLSMTISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFQWQRYW 300
Qy 301 VKGEKTSSP 309
Db 301 VKGEKTSSP 309

RESULT 6

US-10-724-208-8

; Sequence 8, Application US/10724208
; Publication No. US20040209313A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/724,208
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-724-208-8

Query Match 100.0%; Score 1597; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.9e-139;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
Db 1 MITFLPIIFSSLVVTTFVIGNFANGFIALVNSIEWFKQKISFADQILTALAVSRVGLLW 60
Qy 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
Db 61 VLLLNWYSTVLNPAFNSVEVTTAYNIWAVINHFSNWLATLTSIFYLLKIANFSNFIPLH 120
Qy 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVILVMLLGPPLLFLACHLFPVINNNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Qy 181 MVANLVPPTLLTLLSFMLLICSCLKHLKKQQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240
Db 181 MVANLVPPTLLTLLSFMLLICSCLKHLKKQQLHGKSGDPSPTKVHIKALQTVISFLLCAI 240
Qy 241 YFLSMTISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFQWQRYW 300
Db 241 YFLSMTISVWSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQTFLSVFQWQRYW 300
Qy 301 VKGEKTSSP 309
Db 301 VKGEKTSSP 309

RESULT 7

US-10-770-127-179
; Sequence 179, Application US/10770127
; Publication No. US20040214239A1
; GENERAL INFORMATION:
; APPLICANT: SERVANT, GUY
; APPLICANT: OZECK, MARK
; APPLICANT: BRUST, PAUL
; APPLICANT: XU, HONG
; TITLE OF INVENTION: FUNCTIONAL COUPLING OF T1RS AND T2RS BY GI PROTEINS
; TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF T1R
; FILE REFERENCE: 100337.54281US
; CURRENT APPLICATION NUMBER: US/10/770,127
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/444,172
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/457,318
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179
; LENGTH: 309
; TYPE: PRT

PRIOR APPLICATION NUMBER: 60/195,532
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/247,014
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-882-20

Query Match 90.2%; Score 1440; DB 3; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MITPLPIIFSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
Db 1 MITPLPIIFSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
Qy 61 VLLNWYSTVLNPAFNSVEVETAYNIWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Db 61 VLVNMYATELNPAPNSIEVITAYNVWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Qy 121 LKRRVKSIVLMLGPLLFLACHLFLVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVLMLGPLLFLACHLFLVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Qy 181 MVANLVPPTLLSLFMLLICSCLKHLKQWLHGKGSQDPSKVKHKAQTIVISFLLCAI 240
Db 181 ILANLVPPTLLSLFMLLICSCLKHLKQWLHGKGSQDPSKVKHKAQTIVISFLLCAI 240
Qy 241 YFLSIMISVMSFSGLENKPVFMFCKAIRFSPSYHPFILLIWNKCLKKQTFLSVFMQRYW 300
Db 241 YFLSIIMSVMSFSGLENKPVFMFCEATAFSPSTHPFILLIWNKCLKKQTFLSVLMHVRW 300
Qy 301 VKGEKTS 308
Db 301 VKGEKPS 308

RESULT 11

US-10-017-161-1932
Sequence 1932, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ASAI, KIYOSHI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1932
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-161-1932

Query Match 90.2%; Score 1440; DB 4; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MITPLPIIFSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
Db 1 MITPLPIIFSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
Qy 61 VLLNWYSTVLNPAFNSVEVETAYNIWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120

Db 61 VLVNMYATELNPAPNSIEVITAYNVWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Qy 121 LKRRVKSIVLMLGPLLFLACHLFLVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVLMLGPLLFLACHLFLVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Qy 181 MVANLVPPTLLSLFMLLICSCLKHLKQWLHGKGSQDPSKVKHKAQTIVISFLLCAI 240
Db 181 ILANLVPPTLLSLFMLLICSCLKHLKQWLHGKGSQDPSKVKHKAQTIVISFLLCAI 240
Qy 241 YFLSIMISVMSFSGLENKPVFMFCKAIRFSPSYHPFILLIWNKCLKKQTFLSVFMQRYW 300
Db 241 YFLSIIMSVMSFSGLENKPVFMFCEATAFSPSTHPFILLIWNKCLKKQTFLSVLMHVRW 300
Qy 301 VKGEKTS 308
Db 301 VKGEKPS 308

RESULT 12

US-10-292-798-1584
Sequence 1584, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1584
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-798-1584

Query Match 90.2%; Score 1440; DB 4; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MITPLPIIFSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
Db 1 MITPLPIIFSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQILTALAVSRVGLLW 60
Qy 61 VLLNWYSTVLNPAFNSVEVETAYNIWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Db 61 VLVNMYATELNPAPNSIEVITAYNVWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Qy 121 LKRRVKSIVLMLGPLLFLACHLFLVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVLMLGPLLFLACHLFLVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Qy 181 MVANLVPPTLLSLFMLLICSCLKHLKQWLHGKGSQDPSKVKHKAQTIVISFLLCAI 240
Db 181 ILANLVPPTLLSLFMLLICSCLKHLKQWLHGKGSQDPSKVKHKAQTIVISFLLCAI 240
Qy 241 YFLSIMISVMSFSGLENKPVFMFCKAIRFSPSYHPFILLIWNKCLKKQTFLSVFMQRYW 300
Db 241 YFLSIIMSVMSFSGLENKPVFMFCEATAFSPSTHPFILLIWNKCLKKQTFLSVLMHVRW 300
Qy 301 VKGEKTS 308
Db 301 VKGEKPS 308

```
RESULT 13
US-10-724-208-20
; Sequence 20, Application US/10724208
; Publication No. US20040209313A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/724,208
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-724-208-20

Query Match      90.2%; Score 1440; DB 4; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MITPLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
Db 1 MITPLPIIFSSILIVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
Qy 61 VLLNMYSTVLNPAFNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Db 61 VLVLNMYATELNPAPNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNLIPLH 120
Qy 121 LKRRVKSIVLVMILGPLLFLACHLFPVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVLVILLGPLLFLVCHLFPVINNMNQIITWKEYEGNTWKIKLSAMYSNMTVT 180
Qy 181 MVANLVPPTLLSFMLLICSLCKHLKMQQLHGKSGDPSPTKVHIKALQTVTSFLLLCAL 240
Db 181 ILANLVPPTLLISFLLILCSLCKHLKMQQLHGKSGDPSMKVHIKALQTVTSFLLLCAL 240
Qy 241 YFLSIMISVMSFSGLENKPVFMFCKAIRPSYPSIHPFILIWGNKKLKOTFLSVFQMRYW 300
Db 241 YFLSIMSVMSFSGLENKPVFMFCEAIAFSYPSIHPFILIWGNKKLKOTFLSVLHVRYW 300
Qy 301 VKGEKTSS 308
Db 301 VKGEKPSS 308

RESULT 14
US-10-724-209-20
; Sequence 20, Application US/10724209
; Publication No. US20040248149A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 100337.54075US
; CURRENT APPLICATION NUMBER: US/10/724,209
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-724-209-20

Query Match      90.2%; Score 1440; DB 4; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MITPLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
Db 1 MITPLPIIFSSILIVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
Qy 61 VLLNMYSTVLNPAFNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Db 61 VLVLNMYATELNPAPNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNLIPLH 120
Qy 121 LKRRVKSIVLVMILGPLLFLACHLFPVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVLVILLGPLLFLVCHLFPVINNMNQIITWKEYEGNTWKIKLSAMYSNMTVT 180
Qy 181 MVANLVPPTLLSFMLLICSLCKHLKMQQLHGKSGDPSPTKVHIKALQTVTSFLLLCAL 240
Db 181 ILANLVPPTLLISFLLILCSLCKHLKMQQLHGKSGDPSMKVHIKALQTVTSFLLLCAL 240
Qy 241 YFLSIMISVMSFSGLENKPVFMFCKAIRPSYPSIHPFILIWGNKKLKOTFLSVFQMRYW 300
Db 241 YFLSIMSVMSFSGLENKPVFMFCEAIAFSYPSIHPFILIWGNKKLKOTFLSVLHVRYW 300
Qy 301 VKGEKTSS 308
Db 301 VKGEKPSS 308

RESULT 15
US-10-986-871-20
; Sequence 20, Application US/10986871
; Publication No. US20050069944A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/986,871
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/825,882
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-871-20

Query Match      90.2%; Score 1440; DB 5; Length 309;
Best Local Similarity 88.3%; Pred. No. 1.8e-124;
Matches 272; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MITPLPIIFSSLVVVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
Db 1 MITPLPIIFSSILIVTVFVIGNFANGFIALVNSIEWFKRQKISFADQIILTALAVSRVGLLW 60
Qy 61 VLLNMYSTVLNPAFNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNFIPLH 120
Db 61 VLVLNMYATELNPAPNSIEVRITAYNVWAVINHFNSNWLATLSIFYLKIANFSNLIPLH 120
Qy 121 LKRRVKSIVLVMILGPLLFLACHLFPVINNMNEIVRTKEPEGNTWKIKLSAMYFSNMTVT 180
Db 121 LKRRVKSIVLVILLGPLLFLVCHLFPVINNMNQIITWKEYEGNTWKIKLSAMYSNMTVT 180
Qy 181 MVANLVPPTLLSFMLLICSLCKHLKMQQLHGKSGDPSPTKVHIKALQTVTSFLLLCAL 240
Db 181 ILANLVPPTLLISFLLILCSLCKHLKMQQLHGKSGDPSMKVHIKALQTVTSFLLLCAL 240
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|----|-----|---|-----|
| Qy | 241 | YFLSIMISVMSFGSLENKPVFMFCFAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMYW | 300 |
| Db | 241 | YFLSIIMSVMSFESLENKPVFMFCFAIRFSYPSIHPFILIWGNKKLKQTFLSVFWQMYW | 300 |
| Qy | 301 | VKGEKTS | 308 |
| Db | 301 | VKGEKPSS | 308 |

Search completed: April 27, 2006, 21:21:48
Job time : 122 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 27, 2006, 21:19:46 ; Search time 44 Seconds
(without alignments)
319.379 Million cell updates/sec

Title: US-09-825-882-8

Perfect score: 1597

Sequence: 1 MITFLPIFSLVVTFFVG.....FLSVFMQRYVWVGKTSPP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDSS7prodatal/pubpaa/US08_NEW_PUB.pap.*
- 2: /SIDSS7prodatal/pubpaa/US06_NEW_PUB.pap.*
- 3: /SIDSS7prodatal/pubpaa/US07_NEW_PUB.pap.*
- 4: /SIDSS7prodatal/pubpaa/PCT_NEW_PUB.pap.*
- 5: /SIDSS7prodatal/pubpaa/US09_NEW_PUB.pap.*
- 6: /SIDSS7prodatal/pubpaa/US10_NEW_PUB.pap.*
- 7: /SIDSS7prodatal/pubpaa/US11_NEW_PUB.pap.*
- 8: /SIDSS7prodatal/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 695 | 43.5 | 148 | 7 | US-11-264-096-1287 |
| 2 | 459 | 28.7 | 307 | 7 | US-11-264-096-688 |
| 3 | 388 | 24.3 | 111 | 7 | US-11-000-463-330 |
| 4 | 388 | 24.3 | 111 | 7 | US-11-000-463-802 |
| 5 | 287 | 18.0 | 63 | 7 | US-11-264-096-860 |
| 6 | 278 | 17.4 | 318 | 7 | US-11-182-942-2 |
| 7 | 242 | 15.2 | 181 | 7 | US-11-264-096-689 |
| 8 | 130.5 | 8.2 | 380 | 7 | US-11-210-139-17 |
| 9 | 123 | 7.7 | 360 | 6 | US-10-959-310-36 |
| 10 | 123 | 7.7 | 360 | 7 | US-11-144-731-1 |
| 11 | 123 | 7.7 | 360 | 7 | US-11-262-284-34 |
| 12 | 116.5 | 7.3 | 316 | 7 | US-11-188-298-12382 |
| 13 | 116 | 7.3 | 346 | 6 | US-10-455-772-442 |
| 14 | 116 | 7.3 | 346 | 6 | US-10-455-772-444 |
| 15 | 116 | 7.3 | 346 | 7 | US-11-157-930-2 |
| 16 | 113.5 | 7.1 | 318 | 6 | US-10-055-877-324 |
| 17 | 111.5 | 7.0 | 310 | 6 | US-10-455-772-124 |
| 18 | 111.5 | 7.0 | 313 | 6 | US-10-055-877-234 |
| 19 | 111.5 | 7.0 | 316 | 7 | US-11-188-298-9290 |
| 20 | 106.5 | 6.7 | 352 | 7 | US-11-028-922A-1 |
| 21 | 105.5 | 6.6 | 270 | 6 | US-10-455-772-132 |
| 22 | 105.5 | 6.6 | 274 | 6 | US-10-455-772-126 |
| 23 | 105.5 | 6.6 | 318 | 6 | US-10-055-877-119 |
| 24 | 105.5 | 6.6 | 318 | 6 | US-10-055-877-322 |
| 25 | 105.5 | 6.6 | 359 | 6 | US-10-995-561-712 |

| | | | | | | |
|----|-------|-----|-----|---|----------------------|-------------------|
| 26 | 105.5 | 6.6 | 359 | 6 | US-10-995-561-716 | Sequence 716, App |
| 27 | 105.5 | 6.6 | 359 | 7 | US-11-127-877-65 | Sequence 65, Appl |
| 28 | 105.5 | 6.6 | 388 | 6 | US-10-995-561-713 | Sequence 713, App |
| 29 | 105.5 | 6.6 | 394 | 6 | US-10-995-561-714 | Sequence 714, App |
| 30 | 105.5 | 6.6 | 394 | 6 | US-10-995-561-715 | Sequence 715, App |
| 31 | 105.5 | 6.6 | 509 | 7 | US-11-098-686-10325 | Sequence 10325, A |
| 32 | 104 | 6.5 | 362 | 7 | US-11-079-463-6266 | Sequence 6266, Ap |
| 33 | 103.5 | 6.5 | 314 | 6 | US-10-455-772-130 | Sequence 130, App |
| 34 | 103.5 | 6.5 | 314 | 7 | US-11-190-188-16 | Sequence 16, Appl |
| 35 | 103.5 | 6.5 | 321 | 6 | US-10-455-772-128 | Sequence 128, App |
| 36 | 103.5 | 6.5 | 717 | 7 | US-11-096-568A-31003 | Sequence 31003, A |
| 37 | 103.5 | 6.5 | 729 | 7 | US-11-096-568A-31002 | Sequence 31002, A |
| 38 | 103 | 6.4 | 348 | 6 | US-10-330-773-921 | Sequence 921, App |
| 39 | 102.5 | 6.4 | 359 | 6 | US-10-876-787-2 | Sequence 2, Appli |
| 40 | 101 | 6.3 | 463 | 7 | US-11-087-099-1578 | Sequence 1578, Ap |
| 41 | 101 | 6.3 | 463 | 7 | US-11-045-004-1257 | Sequence 1257, Ap |
| 42 | 100.5 | 6.3 | 311 | 6 | US-10-455-772-556 | Sequence 556, App |
| 43 | 100.5 | 6.3 | 311 | 6 | US-10-455-772-570 | Sequence 570, App |
| 44 | 100.5 | 6.3 | 313 | 6 | US-10-455-772-554 | Sequence 554, App |
| 45 | 100.5 | 6.3 | 313 | 6 | US-10-455-772-562 | Sequence 562, App |

ALIGNMENTS

RESULT 1

US-11-264-096-1287
; Sequence 1287, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1287
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1287

| | | | | |
|-----------------------|-------|---|-------|----------------|
| Query Match | 43.5% | Score 695; | DB 7; | Length 148; |
| Best Local Similarity | 89.2% | Pred. No. 8.9e-53; | | |
| Matches | 132; | Conservative | 6; | Mismatches 10; |
| Indels | 0; | Gaps | 0; | |
| Qy | 162 | MTWKIKLKSAMYSFNSMTVTWVANLVPTLTLLSPMLLICSICXHLKXQLHKGSGQDPST | 221 | |
| Db | 1 | MTWKIKLSAVYLSDATVTTGLNVLVPTLTLLCFLLLICSLCKHLKXQLHKGSGQDPST | 60 | |
| Qy | 222 | KVHIKALQTVISFLLCAIYFLSLMISVWSFGSLNKVPMFCFAIRPSYIHPFTLIW | 281 | |
| Db | 61 | KVHIKVLQTVIFFLLCAIYFLSLMISVWSFGSLNKVPMFCFAIRPSYIHPFTLIW | 120 | |
| Qy | 282 | GNKKLKQTFLSVFMQRYVWVGKTSPP | 309 | |
| Db | 121 | GNKKLKQTFLSVLRQRYVWVGKTSPP | 148 | |

RESULT 2

US-11-264-096-688
; Sequence 688, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:


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; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 802
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-802

Query Match      24.3%; Score 388; DB 7; Length 111;
Best Local Similarity 80.9%; Pred. No. 1.5e-26;
Matches 76; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 209 MQLHGKSGDSTKVKHIKALQTVISFLLLCAYFLSIMISWMSFGSLENKPVFMFCKAIR 268
Db 1 MQLHGKSGDSTKVKHIKALQTVISFLLLCAYFLSIMISWMSFGSLENKPVFMFCKAIR 60

Qy 269 FSYPSIHPFLLIWNKKLQKTFSLVFWQMRVYWK 302
Db 61 FSYPSIHPFLLIWNKKLQKTFSLVFWQMRVYWK 94

RESULT 5
US-11-264-096-860
; Sequence 860, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR FILING DATE: 2005-11-02
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 860
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-860

Query Match      18.0%; Score 287; DB 7; Length 63;
Best Local Similarity 93.7%; Pred. No. 4e-18;
Matches 59; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MITFLPIFSLVVVTFVIGNFANGFIALVNSIEWFKRKISFADQILITALAVSRVGLLW 60
Db 1 MITFLPIFSLVVVTFVIGNFANGFIALVNSIEWFKRKISFADQILITALAVSRVGLLW 60

Qy 61 VLL 63
Db 61 VLL 63

RESULT 6
US-11-182-942-2
; Sequence 2, Application US/11182942
; Publication No. US20060019346A1
; GENERAL INFORMATION:
; APPLICANT: Senomyx, Inc.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Tang, Huixian
; APPLICANT: Pronin, Alexey
; TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76
; FILE REFERENCE: 78003-292936
; CURRENT APPLICATION NUMBER: US/11/182,942

; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-942-2

Query Match      17.4%; Score 278; DB 7; Length 318;
Best Local Similarity 28.1%; Pred. No. 1.3e-16;
Matches 84; Conservative 60; Mismatches 135; Indels 20; Gaps 7;

Qy 7 IIFSLVVVTFVIGNFANGFIALVNSIEWFKRKISFADQILITALAVSRVGLLWVLLNW 66
Db 18 IILVTILLRLVAIGNGFITAAALGVWEVLRRLMLPCDLVLSLGSASRFCLQSVVMGKT 77

Qy 67 YSTVLPN---AFNSVEVTRTAYNIWAVINHSNWLATLTLSPYLLKIANFNSFIHLKR 123
Db 78 IYVFLHPMAFFYFNV-LQFLAQ-WDFLNAATLWSSTWLSVFCVKIATFTHPVFWLKH 135

Qy 124 RVKSVILVMLGP-----LLFLACHLFPVINNNEIVRTKEPEGNMTWKIKLSAMYF 174
Db 136 KLSGWLPMFLFSSVGLSSFTTILFFIGNHMYQN---YLRNHLQFVWNVIGDSIRSCEKF 192

Qy 175 SNMTVTVMANLVPFTLLSLFMLLCSLCKHLKQMLHGKSGDSTKVKHIKALQTVISF 234
Db 193 YLPLKMITWTMTPTAVFFICMILLITSLGRHKALLTTSGRFSPVQAHIKALLALSP 252

Qy 235 LLLCAIYFLSIMISWMS-FGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQKTFLS 292
Db 253 AMLFISYFLSLVSAAGIFPPPLDFK--FWWMSVIYLCAAVHPITLLFNSCRLRAVLKS 309

RESULT 7
US-11-264-096-689
; Sequence 689, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR FILING DATE: 2005-11-02
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 689
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-689

Query Match      15.2%; Score 242; DB 7; Length 181;
Best Local Similarity 32.2%; Pred. No. 9.1e-14;
Matches 55; Conservative 40; Mismatches 70; Indels 6; Gaps 1;

Qy 128 VILVMLGLPLLFLACHLFPVINNNEIVRTKEPEGNMTWKIKLSAMYFSNMTVTVMANLVP 187
Db 6 MIVFLLISLNLFA-----YIAKLNDYKDKNDTVDLNNMYSEYFIKQILLNLGVIFF 59

Qy 188 FTLTLISFMLLISLCKHLKQMLHGKSGDSTKVKHIKALQTVISFLLIYFLSLIMI 247
Db 60 FTLTLITCIFIILSLWHRNQMSNVTLGRSDNTAEHVAKMKVLISFILFIYFIGNAI 119

Qy 248 SVMSFGSLENKPVFMFCKAIRFSYPSIHPFILLIWNKKLQKTFLSVFWQMR 298
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1 APPLICATION: ARABID, MARK S. ET AL.
 2
 3 TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 4
 5 FILE REFERENCE: 38-21(53452)B
 6
 7 CURRENT APPLICATION NUMBER: US/11/188,298
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Search completed: April 27, 2006, 21:22:43
Job time : 44 secs

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| Result No. | Score | Query % | | | ID | Description |
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| | | Match | Length | DB | | |
| 1 | 677.2 | 72.8 | 2418 | 4 | AF1161728 | AF1161728 Homo sapi |
| C 2 | 674.6 | 72.5 | 699 | 9 | BZ604233 | BZ604233 WHADD11TF |
| C 3 | 460.6 | 49.5 | 790 | 7 | C0595975 | C0595975 AGENCOURT |
| . | 378 | 40.6 | 569 | 8 | DN997644 | DN997644 TC102961 |
| | 340.8 | 36.6 | 554 | 11 | DQ040209 | DQ040209 Homo sapi |
| | 336.8 | 36.2 | 554 | 1 | AL037695 | AL037695 DKF2P5640 |
| C 6 | 336.8 | 32.8 | 500 | 10 | CE692204 | CE692204 tigr-gss- |
| C 8 | 294.8 | 31.7 | 796 | 11 | DQ040210 | DQ040210 Pan trogl |
| C 9 | 293.6 | 31.6 | 397 | 9 | AG164951 | AG164951 HS_3014_B |
| 10 | 284.4 | 30.6 | 466 | 9 | B17827 | B17827 347L19.TPB |
| C 11 | 276.6 | 29.7 | 870 | 11 | CR071716 | CR071716 Forward s |
| C 12 | 267.6 | 28.8 | 677 | 2 | BG402330 | BG402330 602465915 |
| 13 | 256.4 | 27.6 | 761 | 11 | DQ040211 | DQ040211 Homo sapi |
| 14 | 252.2 | 27.1 | 330 | 1 | AN266498 | AN266498 ZG24_gasc |
| 15 | 248 | 26.7 | 711 | 7 | C0926496 | C0926496 AGENCOURT |
| 16 | 246.6 | 26.5 | 711 | 6 | CF147793 | CF147793 AGENCOURT |
| 17 | 232.8 | 24.0 | 697 | 10 | CZ406953 | CZ406953 1002656_R |
| 18 | 220 | 23.7 | 957 | 11 | DQ040217 | DQ040217 Homo sapi |
| 19 | 215.2 | 23.1 | 752 | 8 | DN693348 | DN693348 AGENCOURT |
| 20 | 208.6 | 22.4 | 924 | 11 | DQ040213 | DQ040213 Homo sapi |
| 21 | 198.2 | 21.3 | 924 | 11 | DQ040214 | DQ040214 Pan trogl |
| 22 | 193.4 | 20.8 | 741 | 10 | AG374557 | AG374557 Mus muscu |

| | | | | | | | | | |
|-----------------------|-------|---|----------|------------|-----|--------|------|------|---|
| ORIGIN | | | | | | | | | |
| Query Match | 72.8% | Score | 677.2 | DB | 4 | Length | 2418 | | |
| Best Local Similarity | 83.0% | Pred. No. | 9.4e-168 | | | | | | |
| Matches | 772 | Conservative | 0 | Mismatches | 158 | Indels | 0 | Gaps | 0 |
| Qy | 1 | ATGATAACATTTTCTACCCATCATTTTTTCAGTCTGCTAGTGGTTCACATTTGTTATTGGA | 60 | | | | | | |

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Db 930 ATGGTATATTTCTGCTCATCATTTTATCAATTTCTGGTAGTGTGTCATTTGTCATTTGTTCTTGA 989
Qy 61 AATTTTGTATAGGCTTCATAGCATCTGGTAATTCATTTAGTGTGTTCAAGAGACAAAG 120
Db 990 AATTTTCCAATGGCTTCATAGCTCTAGTAATATGTCAATGACTGGTTAAAGACACAGAAAG 1049
Qy 121 ATCTCTCTTTGTCAGCAAAATTTCTACTGCTCTGGGGGCTCCAGAGTTGGTTGCTCTGG 180
Db 1050 ATCTCTCTGCTGACCAAAATCTCACTGCTCTGGGGGCTCCAGAAATTTGTTTACTCTGG 1109
Qy 181 GTATTATTATTAACCTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 1110 GTCAATATTATTAATTTGGTATGCAATGTGTTTAAATTCAGCTTTATATAGTTTCAAGTA 1169
Qy 241 AGAACTACTGCTTATAATATCTGGGAGTGTATCAACATTTTCCAGCAACTGGCTTGTCTACT 300
Db 1170 GGAGCTGTGCTTCTAATATCTCAGCAATAATCAACCAATTTTCCAGCATCTGGCTTGTCT 1229
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCCAACTTTTATTTTCTTCCAC 360
Db 1230 AGCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTCTCCAACTTTTATTTTCTTCCAC 1289
Qy 361 TTAAGAGAGAGATTAAGAGTGTCAATCTGTGTGATGTTGTTGGGGCTTTTGTCTATTTTGG 420
Db 1290 CTAAGAGAGAGATTAAGAGTGTGTTCTGGTGATCTGTTGGGTCCTTGGTATTTTGG 1349
Qy 421 GCTTGTCTATCTTTTGTGTATAAATCAATGATGATTTGGCGGACAAAGAAATTTGAAGA 480
Db 1350 ATTTGTAAATCTTGTGTGTATAAATCAATGATGATGATTTGGCGGACAAAGAAATTTGAAGA 1409
Qy 481 ACATGACTTGAAGATCAAAATTTGAAGTGTCAATGATGATTTTCAAAATATGATCTTAACC 540
Db 1410 AATGTGACTTGGAAAGATCAAAATTTGAAGTGTCAATGATGATTTTCAAACTTTGACTGTAGC 1469
Qy 541 ATGTGTAGCAAACTTAGTACCTTTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGT 600
Db 1470 ACATAGCAAACTCATACCTTTCACTCTGACCTAATATGTTTCTGCTGTTAATCTGT 1529
Qy 601 TCTTTGTGTAAATCTCAAGAGATGCAAGCTCCATGTTAAAGGATCTCAAGATCCAGC 660
Db 1530 TCTGTGATAAATCTCAAGAGATGCAAGCTCCATGTTAAAGGATCTCAAGATCTCAGC 1589
Qy 661 ACCAAGTCCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTGTTATGTGCTCAT 720
Db 1590 ACCAAGTCCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTGTTATGTGCTCAT 1649
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Qy 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCTCTCAATCCACCCATTCATCTGATT 840
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Qy 841 TGGGAAACAAAGACTAAGCAGACTTTTCTTTCAGTTTTCAGTTTTCAGTTTTCAGTTCATGCTTA 1829
Db 1770 ATGGGAGAGAGAACTAAACAGAGCTTTCTTTCAGTTTTCAGTTCATGCTTA 1829
Qy 901 GTGAAGAGAGAGAACTTTCATCTCCATAG 930
Db 1830 GTGAAGAGAGAGAACTTTCATCTCCATAG 1859
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RESULT 2
BZ604233/c
LOCUS WHADD11TF Human MCF7 breast cancer cell line library (MCF7_1) Homo
DEFINITION sapiens genomic clone MCF7_1-19B22, genomic survey sequence.
ACCESSION BZ604233
VERSION BZ604233.1 GI:31512695
KEYWORDS GSS.
SOURCE Homo sapiens (human)
. ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 699)
Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q.,
Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P.,
Gray, J.W. and Collins, C.
Gray, J.W. and Collins, C.
End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
12788976

CONTACT: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com

CLASS: BAC ends.
LOCATION/Qualifiers
1..699
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_1-19B22"
/sex="female"
/clone_lib="Human MCF7 breast cancer cell line library (MCF7_1)"
/note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

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Query Match 72.5%; Score 674.6; DB 9; Length 699;
Best Local Similarity 99.4%; Pred. No. 3.4e-167;
Matches 677; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGATAACTTTTACCCATCATTTTTTCCAGTCTGGTAGTGTGTTTACATTTGTTTGA 60
Db 681 ATGATAACTTTTACCCATCATTTTTTCCAGTCTGGTAGTGTGTTTACATTTGTTTGA 622
Qy 61 AATTTTGTATAGGCTTCATAGCATCTGTAATTCATTTAGTGTGTTCAAGAGACAAAG 120
Db 621 AATTTTGTATAGGCTTCATAGCATCTGTAATTCATTTAGTGTGTTCAAGAGACAAAG 562
Qy 121 ATCTCTTTGCTGACCAAAATTTCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 561 ATCTCTTTGCTGACCAAAATTTCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 502
Qy 181 GTATTATTATTAACCTGGTATTCATCTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 501 GTATTATTATTAACCTGGTATTCATCTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 442
Qy 241 AGAACTACTGCTTATAATATCTGGCAGTGTATCAACCACTTTTCAAGAACTGCTACT 300
Db 441 AGAACTACTGCTTATAATATCTGGCAGTGTATCAACCACTTTTCAAGAACTGCTACT 382
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCAATTTTCTCCAACTTTTATTTTCTTCC 360
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Qy 361 TTAAGAGAGAGATTAAGAGTGTCAATCTGTGTGATGTTGTTGGGGCTTTTGTCTATTTTGG 420
Db 321 TTAAGAGAGAGATTAAGAGTGTCAATCTGTGTGATGTTGTTGGGGCTTTTGTCTATTTTGG 262
Qy 421 GCTTGTCTATCTTTTGTGTATAAATCAATGATGATGATTTGGCGGACAAAGAAATTTGAAGA 480
Db 261 GCTTGTCTATCTTTTGTGTATAAATCAATGATGATGATTTGGCGGACAAAGAAATTTGAAGA 202
Qy 481 AACATGACTTGAAGATCAAAATTTGAAGAGTGTCAATGATGATTTTCAAAATATGATCTGAACC 540

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Db      201 AACATGACTTGGAGATCAAAATTTGAAGTGCATGTAATTTTCAATATGACTGTGAACC 142
Qy      541 ATGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
Db      141 ATGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 82
Qy      601 TCTTTGTGTAACATCTCAAGAAGATGAGTCCATGTTAAAGGATCTCAAGATCCCGAC 660
Db      81 TCTTTGTGTAACATCTCAAGAAGATGAGTCCGTTGTTAAAGGATCTCAAGATCCCGAC 22
Qy      661 ACCAAGTTCACATATAAAGCT 681
Db      21 ACGAAGTCCACATATAAAGCT 1

RESULT 3
CO959975/c
LOCUS
DEFINITION
AGENCOURT_30842526 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7389866 3', mRNA sequence.
CO959975
CO959975.1 GI:51324548
EST.
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 790)
NITH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NITH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB18 row: h column: 12
High quality sequence start: 28
High quality sequence stop: 600.
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1..790
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/clone_lib="NIH_MGC_145"
/notes="vector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NITH_MGC Library."

ORIGIN
Query Match 49.5%; Score 460.6; DB 7; Length 790;
Best Local Similarity 80.8%; Pred. No. 1.5e-110;
Matches 572; Conservative 0; Mismatches 132; Indels 4; Gaps 3;
Qy      196 TGGTATTCACTGTTGATCCAGCTTTTAAATAGTGTAGAGTAAAGTACTGCTTAT 255
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Db      745 TGGTATGCACCTGTGTTAATTC--TGCTTTATATGGTTAGAAAGTAAGAA--TGTGCTTTNT 689
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Db      688 AATCGNTGGGCTGTAAAGAACATTTTCAAGCATGTGGC--TGCTGTAGCTTCAAGCATATTT 630
Qy      316 TATTGCTCAAGATGCAATTTCTCCAACTTTATTTTCTTCACTTAAAGAGGAGTT 375
Db      629 TGTGTTGCTCAAGATGCAATTTCTCCAACTTTATTTCTCTCCACTTAAAGAGAAAT 570
Qy      376 AAGAGTGTCTTCTGTTGATGTTGTTGGGCTTTGCTATTTTGGCTTGTGTCATCTTTT 435
Db      569 AAGAGTGTGTTCTGTTGATGTTGTTGGGCTTTGTTGTTTCTGTTTGTAAATCTTGTCT 510
Qy      436 GTGATAAACATGAATGAGATTGTGGGACAAAAGAAATTTGAAGGAAAACATGACTTTGGAAG 495
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Qy      556 GTACCCCTTCACTCTGACCTACTATCTTTTATGCTTGTAAATCTGTTCTTTGTGTAACAT 615
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Qy      616 CTCAAGAAGATGCAAGTCCATGTTAAAGATCTCAAGATCCAGCAACCAAGTCCACATA 675
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Qy      676 AAAGCTTTGCAAACTGTGATCTCTCTCTCTGTTGTTATGTCGCAATTTACTTCTGTCCATA 735
Db      269 AAAGCTTTGCAAACTGTGACCTCTCTCTCTGTTATTTATTTGTCATTTACTTCTGTGTATA 210
Qy      736 ATGATATCAGTTGGAGTCTTGGAGTCTGGAACCAAAACCACTCTTCTCATGTTCTGCAAA 795
Db      209 ATCACATCAACTTGGAACTTTAGGACACAGCAGAGCAAACTTGTACTCTGCTTTGGCAA 150
Qy      796 GCTATTAGATTCAGCTATCTTCAATCCACCATTCATCTCTGATTGGGGAACAAAGAAAG 855
Db      149 ACTGTTGCAATCATGATCTCTTCAATCCACTCATTCCTGATTATGGAAGTAGGAAG 90
Qy      856 CTAAAGCAGACTTTCTTCTGATTTTGGCAAAATGAGGTACTGGGTG 903
Db      89 CTAAACAGACCTTTCTTCTGATTTTGTGGCAGATGACACGCTGAGCG 42

RESULT 4
DN997644
LOCUS
DEFINITION
DN997644.1 GI:66257471
EST.
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 569)
Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Zhang, X., Jay, G. and He, W.
High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
Contact: Kovacs, KF
High Throughput cDNA Cloning
Origene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA

```

Tel: 301 340 3188
 Fax: 301 340 8606
 Email: cdna@origene.com
 This EST submission is part of an on-going human full-length
 cloning project at Origene Technologies, Inc.
 Please contact Origene for access.
 Origene Technologies, Inc.
 6 Taft Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com
 Seq primer: pCMV6 5prime forward vector primer, Origene
 Technologies Inc.

FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TC102961"
 /tissue_type="Breast cancer"
 /clone_lib="Human breast cancer tissue, large insert, pCMV
 expression library"
 /note="Organ: Mammary gland (cancer tissue); Vector:
 pCMV6-XL5; Site 1: EcoRI; Site 2: XhoI/Sall compatible end
 ligatio; Oligo-dT primed reverse transcription optimized
 for large and GC rich mRNA transcripts, cDNA size
 selection, optimized ligation for large inserts into
 mammalian expression vector, random clones selected for
 end sequence verification of full-length genes"

ORIGIN

Query Match 40.6%; Score 378; DB 8; Length 569;
 Best Local Similarity 94.0%; Pred. No. 1e-88;
 Matches 393; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 ATGATAACTTTTCTACCCCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
 DB 152 ATGATAACTTTTCTGCCCATCATATTTCCATCTAGTAGTGGTTACATTTGTTATTGGA 211
 QY 61 AATTTGCTAATGGCTTCATAGACATGTTAAATTCATTGATGGTTCAGAGACAAAAG 120
 DB 212 AATTTGCTAATGGCTTCATAGCGTTGGTAAATTCACCGAGTGGTGAAGACAAAAG 271
 QY 121 ATCTCCTTTGCTGACCAATTCCTACTGCTCTGGGGTCTCCAGAGTGGTTGCTCTGG 180
 DB 272 ATCTCCTTTGCTGACCAATTTGCTACTGCTCTGGGGTCTCCAGAGTGGTTGCTCTGG 331
 QY 181 GTATTATTATTAACTGGTATTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
 DB 332 GTGTTATTATTAAATGGTATTCAACTGTGTTGAATCCAGCTTTTGTAGTGTAGATTGA 391
 QY 241 AGAATCTAGCTTATAATATCTGGGAGTGATCAACCATTTGAGCACTGGCTTGTCTACT 300
 DB 392 AGAATCTAGCTTATAATATCTGGGAGTGAACCGGCATTTGAGCACTGGCTTGTCTACT 451
 QY 301 ACCCTCAGCATATTTATTGCTCAAGATTGCCAATTTCTCCAACTTTATTTTCTTCAC 360
 DB 452 AGCCTCAGCATATTTATTGCTCAAGATTGCCAATTTCTCCAACTTTATTTTCTTCGC 511
 QY 361 TTAAGAGAGAGAGTTAAGAGTGTCAATTCCTGGTGATGTTGTTGGGGCTTTGCTATTTT 418
 DB 512 TTAAGAGAGAGAGTTAAGAGTGTCAATTCCTGGTGATGTTGTTGGGGCTTTGCTATTTT 569

RESULT 5

LOCUS DQ040209 954 bp DNA linear GSS 02-JUN-2005
 DEFINITION Homo sapiens TAS2R14 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION DQ040209
 VERSION DQ040209.1 GI:66891418
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 AUTHORS 1 (bases 1 to 954)
 Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
 Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
 White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
 TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
 Chimpanzees
 JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
 PUBMED 15869325
 REFERENCE
 AUTHORS 2 (bases 1 to 954)
 Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
 Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
 White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Direct Submissio
 JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment. Translation starts at the beginning of
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 Best Local Similarity 63.6%; Pred. No. 8e-79;
 Matches 589; Conservative 0; Mismatches 322; Indels 15; Gaps 4;
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 DB 9 TGTCTAAGAGCATATTTACATTCGTTTAAATGTGGAAATTAATTTGGAATTTAGG 68
 QY 69 TAATGGCTTCATAGACATCGTAAATTCATTGAGTGGTTCAGAGACAAAAGATCTCCTT 128
 DB 69 AAATAGTTTCATAGACATCGTAAATTCATTGAGTGGTTCAGAGACAAAAGATCTCCTT 128
 QY 129 TGCTGACCAATTTCTACTGCTCTGGCGGTCTCCAGAGTGGTTGCTCTGGGTATTATT 188
 DB 129 GGTTCATCGGATCCTCACTGCTTTGGCAATCTCTCGAATTAGCCCTGGTTGTTAATA 188
 QY 189 ATTAACTGGTATTCAACTGTGTTGAATCCAGCT--TTTAATAGTGTAGAAGTAAGAAC 245
 DB 189 CGGAAGCTGGTGTGTCTGTGTTTTTCCAGCTTTATTTGCCACTGAAATAATGTTTCA 248
 QY 246 TACTGCTTATAATATCTGGCAGTGATCAACCATTTTCAGCACTGGCTTGTCTACCTCT 305
 DB 249 AATGCTTACTAATATCTGGACAGTCAATCAATCATTTTAGTGTCTGGTAGCTACAGCCT 308
 QY 306 CAGCATATTTATTGCTCAAGATTGCCAATTTCTCCAATTTATTATTCTTCTCACTTAA 365
 DB 309 CGGTACTTTTATTATTTCTCAAGATAGCCAAATTTTCTAACTATTTTCTCTACCTAAA 368
 QY 366 GAGGAGAGTTAAGAGTGTCAATTCCTGGTGATGTTGTTGGGGCTTTTGCTATTTTGGCTTG 425
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 QY 426 TCATCTTTTGTGATAAATGAAATGAGATGTGGCGACAAAGAAATTTGAAGAGAAACAT 485
 DB 429 AAATATTGCACGTAAACATCCATATAAATCCAGATATCAATGGATACAGAAGAACAA 488
 QY 486 GACTTGGAGATCAATTTGAAGAGTGCATGTACTTTTCAATATATGACTGTGA----AC 539
 DB 489 GACTTGGAGTCTCTGATTCAGTAATTTTACAGATTTTCCAGTCTTATTGTATTACAC 548


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RESULT 9
AQ164951/c
LOCUS
DEFINITION
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ACCESSION
  AQ164951.1 GI:3563146
VERSION
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1 (bases 1 to 397)
  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
  Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  10449764
COMMENT
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Sequence tagged Connector
  Plate: 3014 row: P column: 14
  Class: BAC ends
  High quality sequence stop: 397.
FEATURES
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      /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
      E-Coli DH10B"
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  Best Local Similarity 83.6%; Pred. No. 2e-66; Indels 0; Gaps 0;
  Matches 332; Conservative 0; Mismatches 65;
Qy 353 TTCTTCACTTAAAGAGGAGGTTAAGAGTGCATTCCTGGTGATGTTGTGGGGCCTTTGC 412
Db 397 TTCATCACTTANAAGGAAGGCTAAGAGTGTAGTTCCTGGTGATAGTGTGGGTCTTTGT 338
Qy 413 TATTTTGGCTGTGCATCTTTTGTGATAAACAATGAGATGTGGGACAAAAGAAT 472
Db 337 TCTTTTGGTTGTCAACTGTGTGATGAAAAACACGTATATAATGTGTGACAGAAGAAT 278
Qy 473 TTGAAGGAAACATGACTTGGGAAGTCAATTTGAAGAGTCAATGACCTTTTCAATATGA 532
Db 277 GTGAAGGAAACGTAACCTTGGGAAGTCAAACTGAGGAGTCAATGACCTTTTCAACTTGA 218
Qy 533 CTGTAACCATGGTAGCAAACTTAGTACCTTCACTCTGACCTCACTATCTTTTATGCTGT 592
Db 217 CTGTAGCCATGCTAGCAAACTTGTATACCATTCACCTCTGACCTGATATCTTTCTGCTGT 158
Qy 593 TAATCTGTTTGTGTAAACATCTCAAGAGATGACGATCGATGTAAGAGATCTCAAG 652
Db 157 TAATCTACTCTGTGTAAACATCTCAAGAGATGACGATCGATGTAAGAGATCTCAAG 98
Qy 653 ATCCAGACCAAGGTCACATAAAGCTTTGCAAACTGTATCTCCCTTCCTCTGTTAT 712
Db 97 ATCCAGACCAAGATCCACATAAAGCTTCGCAAACTGTGACCTCTTCCTCGTATTAC 38

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Qy 713 GTGCCATTTACTTTCTGTCCATAATGATATATCAGTTTG 749
Db 37 TTGCCATTTACTTTCTGTGTCTTAATCATATCCTTTTG 1

RESULT 10
B17827
LOCUS
DEFINITION
  B17827.TPB CIT978SKA1 Homo sapiens genomic clone A-347L19, genomic
  survey sequence.
ACCESSION
  B17827
VERSION
  B17827.1 GI:2125576
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1 (bases 1 to 466)
  Adams,M.D., Kelley,J.M., Rounsley,S.R. and Venter,J.C.
  Use of a BAC End Sequence Database for Sequence-Ready Map Building
  Unpublished (1997)
  Other_GSSs: 347L19.TVB
COMMENT
  Contact: Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: mdadams@tigr.org
  Clones are available from Research Genetics (info@resgen.com). BAC
  end search page:
  http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html
  Seq primer: SP6
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ORIGIN
  Query Match      30.6%; Score 284.4; DB 9; Length 466;
  Best Local Similarity 82.2%; Pred. No. 5.7e-64;
  Matches 327; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
Qy 533 CTGTAACCATGGTAGCAAACTTAGTACCTTCACTCTGACCTCACTATCTTTTATGCTGT 592
Db 1 CTGTAACCATCTAGCAAACTTACCTTCTGAGCCTAATATGTTTCTGCTGT 60
Qy 593 TAATCTGTTCTTTGTGTAAACATCTCAAGAGATGACGATCGATGTAAGAGATCTCAAG 652
Db 61 TAATCTGTTCTTTGTGTAAACATCTCAAGAGATGCGGCTCAATGACAGATCTCAAG 120
Qy 653 ATCCAGACCAAGGTCACATAAAGCTTTGCAAACTGTGATCTCTTCCTCTGTTAT 712
Db 121 ATCCAGACCAAGGTCACATAAAGCTTTGCAAACTGTGACCTCTTCCTCATGTTAT 180
Qy 713 GTGCCATTTACTTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAGTCTGGAACA 772
Db 181 TTGCCATTTACTTTCTGTGTATAATCAATCAACTTGGAACTTAGGACACAGAGACA 240
Qy 773 AACCTGTCTTCAATGTTCTGCAAAAGCTATTAGATTCACTATCTTCATCCACCATTTCA 832
Db 241 AACTTGTAATCTCTGCTTTGCCAACTGTGCAATCATGTAATCTTCATTCACACTATCA 300
Qy 833 TCCTGATTTGGGAAACAAGAGCTTAAAGCAGACACTTTTCTTTCAGTTTTCGGCAATGA 892

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||||| 301 TCTGATATTGGAAGTAGGAGCTTAACACAGCCTTCTTTCAGTTTGTGGCAGATGA 360
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893 GGTACTGGGTGAAAGAGAGAGACTTCATCTCCATAG 930
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361 CATGCTGAGTGAAGAGAGAAACCTCAACTCCATAG 398
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RESULT 11
CR071716/c 870 bp DNA linear GSS 05-JUL-2004
LOCUS Forward strand read from insert in 5'HPRT insertion targeting and
DEFINITION chromosome engineering clone MHPN99102, genomic survey sequence.

ACCESSION CR071716.1 GI:49805306
VERSION GSS; genome survey sequence; MICER.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 870)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.

TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES
source

1..870
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN99102"
/clone_lib="MHPN"

ORIGIN

Query Match 29.7%; Score 276.6; DB 11; Length 870;
Best Local Similarity 59.6%; Pred. No. 7.6e-62;
Matches 506; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

QY 43 GTTACATTTGTTATTGGAATTTTGCTAATGGCTTCATAGCACTGGTAAATTCATTTGAG 102
DB 870 GTGGAATTAGTAATTGGAATTATAGGAATGGTTTCATGCTGCTCCACTGTATGGAC 811
QY 103 TGGTTCAAGAGACAAAGATCTCTTTGCTGACCAAAATCTCAGCTGCTCGGGGTCTCC 162
DB 810 TGGGTTAAGAAAAGAAAATGCTCCCTAGTTAATCAAAATCTTACTGCTTTGTCAATCTCC 751
QY 163 AGAGTTGGTTGCTCTGGGTATTATTATTAAGCTGTTTCACTGCTGTTGAATCCAGCT 222
DB 750 AGAATTTTTCAGCTCTGTTATTGTTTATTAAGTTTAGTAATCAACTTTTCATATACAGAT 691
QY 223 TT---TAATAGTGTAGAAGTAAGAAGTACTGCTTATATATATCTGGCAGTGATCAACCAT 279
DB 690 TTAACACAGTTCAGGATGATACAGTCATGACAAAGCTTGGATTTTAGCCAAACCAT 631
QY 280 TTCAGCAACTGGCTGCTACTACCTCAGCATATTTTATTGCTCAAGATTGGCAATTTTC 339
DB 630 TTCAGCATCTGGATTGCTACATGCTCTCACTGCTCTTTATTTTCTTAAAGATAGCAATTTT 571
QY 340 TCCAACTTTATTTTCTTCCATTAAAGAGAGAGTTAAGAGTCTCATCTCTGTTGATGTTG 399
DB 570 TCTAACTCTTTTCTTTCTTATCTAAAGTGAGAGTTGAAAAGTAGTTTCAGTTACACTG 511
QY 400 TTGGGGCCTTTGCTATTTTGGCTTCTCATCTTTTGTGATAAACAATGAATGAGATTGTG 459
DB 510 TTGGTGTCAATGCTCTCTCTGATTATTTAAATATTTTACTAACTTAACCTTGGAAACCGACATG 451
QY 460 CGGACAAAAGAAATTTGAAGAAACATGACTTGGAGATCAATTTGAAGAGTGAATGTATAC 519
DB 450 TGGACAAATGAATATCAAGAAACATATCATGCGCTTCAGTTCTCATTACTATGCAAG 391

QY 520 TTTTCAAATATGACTGTAA-----CCATGGTAGCAAACTTAGTACCCTTCACTCTGACC 573
DB 330 TGTACAGCGAGGTGTTAAGGCTTCACATTAATTTCTGTCTGTCCCGCTTTTGTGTC 331
QY 574 CTACTATCTTTTATGCTGTTAATCTGTTCTTTTGTGTAAACATCTCAAGAAGATGACGCTC 633
DB 330 CTGTCAACTTTTCTCTGCTCATCTCTCCCTGTGGACACATCAACAAGAGGATGACGAC 271
QY 634 CATGTAAGGATCTCAAGATCCAGACCAAGGTCACATATAAAGCTTTGCAAACTGTG 693
DB 270 CATGTTCAAGGAGGAGAGATGCCAAGACCAAGCGGCCACTTCAAAAGCCCTACAAACTGTG 211
QY 694 ATCTCTCTCTCTGTTATGTCCTTACTTTTCTGTCATATGATATGATATGATTTGGAGCT 753
DB 210 ATTGCAATTTTCTTACTATATTCATTTTATCTGCTGCTTATATACAAATTTGGAAA 151
QY 754 TTGGAAGTCTGGAAAAACAACTCTCTTCATGTTCTGCAAGCTATTAGATTCAGCTAT 813
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QY 814 CTTTCAATCCACCCTTTCATCTGATTTGGGGAACAAGAGCTTAAGCAGACTTTTCTT 873
DB 90 CGACATTTCCATTCATATATTTCTGATTGTAGGAGACATGAAGCTGAGACAGGCGCTG 31
QY 874 TCAGTTTTT 882
DB 30 CCTCTCTGT 22

RESULT 12
BG402330
LOCUS 602465915F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4593986 5',
DEFINITION mRNA sequence.

ACCESSION BG402330

VERSION BG402330.1

KEYWORDS GI:13295778

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 677)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1334 row: n column: 03
High quality sequence stop: 636.
Location/Qualifiers
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/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
3' adaptor were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

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ORIGIN
Query Match      28.8%; Score 267.6; DB 2; Length 677;
Best Local Similarity 92.1%; Pred. No. 1.7e-59;
Matches 293; Conservative 0; Mismatches 24; Indels 1; Gaps 1;
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Db 1 CATCTCAAGAAGATCAGCTCCATCGCAAGGATCTCAAGATCCAGACCAAGTCCAC 60
QY 673 ATAAAGCTTTGCAAACTGTGATCTCCTTCCTCTTGTATATGTCATTTCTGTCC 732
Db 61 ATAAAGCTTTGCAAACTGTGATCTCCTTCCTCTTGTATATGTCATTTCTGTCC 120
QY 733 ATATGATATCAGTTTGGAGTTTGGAGTCTGGAAACCAACCTGCTTCATGTTCTGC 792
Db 121 ATGATCATATCAGTTTGTAAATTTTGGAGGCTGGAAAGCAACCTGCTTCATGTTCTGC 180
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Db 181 CAGCTATTATTCAGCTATCCTTCAACCCACCCATTCATCCTGATTTGGGAAACAAG 240
QY 853 AAGCTAAAGCAGCTTTCTTTCAGTTTGTGGCAAAATGAGGTACTGGGTGAAGAGAG 912
Db 241 AAGCTAAAGCAGATTTTCTTTCAGTTTGTGGCATGTGAGGTACTGGGTGAAA-GACAG 299
QY 913 AAGCTTTCATCTCCATAG 930
Db 300 AAGCTTTCGCTCCATAG 317
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RESULT 13
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DEFINITION genomic survey sequence.
ACCESSION DQ040211
VERSION DQ040211.1 GI:66891420
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fladel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 761)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fladel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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ORIGIN
Query Match      27.6%; Score 256.4; DB 11; Length 761;
Best Local Similarity 62.2%; Pred. No. 1.6e-56;
Matches 458; Conservative 0; Mismatches 266; Indels 12; Gaps 3;
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QY 212 TGAATCCAGCT--TTTAAATAGTGTAGAAGTAAGAACTACTGCTTATATATCTGGCAG 268
Db 61 ATTATCTAGCCATATTTGTGCTGGAACAGGAATTAAGAAATTATAGATTTTTAGCTGATAG 120
QY 269 TGATCAACCAATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATTTTATTTTGGCTCAAGA 328
Db 121 TTTCTAATCACTCAATCTCTGGCTTGCTACAATCTTCAGCATCTTTTATTTTGGCTCAAAA 180
QY 329 TTGCCAATTTCTCCAACTTTTATTTTCTTCTTCTTAAAGAGGAGAGTTTAAGAGTGTCAATTC 388
Db 181 TAGCGAGTTTCTTAGCCCTGCTTTTCTTCTATTTTGAAGTGGAGAGTAACAACAAAGTGATTC 240
QY 389 TGGTGATCTGTGGGGCTTTTGTATTTTGGGCTTGTTCATCTTTTGTGATAAATCAATCA 448
Db 241 TGATGATACTGCTAGGAACCTTTGGTCTTCTTATTTTAAATCTGATACAAATAAATCAATGC 300
QY 449 ATGAGATTTGTGGGCAAAAGAAATTTGAAGGAAACATGACCTTTGGAGATCAAAATTTGAAGA 508
Db 301 ATATAAAAGACTGGCTGGACCGATATGAAAGAAACACAACCTTTGGAAATTTCAATATGAGTG 360
QY 509 GTGCAATGTACTTTTCAAATATGACTGTAAACATCGGTAGCAAACTT-----AGTACCCT 562
Db 361 ACTTTGAAACATTTTTCAGTGTGGTCAAAATTCATATGACTATGTTTCACTTAACACCAT 420
QY 563 TCACCTTGACCTTACTATCTTTTATGCTGTAACTGTTCTTTTGTGTAACATCTCAAGA 622
Db 421 TTACTGTGGCTTTCATCTCTTTTCTCTGTTAAATTTTCTCCCTGAGAAACATCTCCAGA 480
QY 623 AGATGCAGCTCCATGTAAAGATCTCAAGATCCCAGCACCAAGGTCCACATAAAAGCTT 682
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QY 683 TGCATAATGATCTCTCTTCTTGTATATGTCATTTTCTTCTGTCATTAATGATAT 742
Db 541 TGAATAATGTGATCTCATCTCTTTTATTTCTATGCTAGTTTCTTCTTCTGTTTCTCATAT 600
QY 743 CAGTTTGGAGTTTGGAGTCTGGAAACAAACCTGTTCTCATGTTCTGCAAGCTATTTA 802
Db 601 CA---TGGATTTCTGAGCTGTATTCAGACACAGTGTATCTACATGCTTTTGTGAGACGATG 657
QY 803 GATTGAGTATCTCTTCAATCCACCCATTCATCCTGATTTGGGAAACAAAGAGCTAAAGC 862
Db 658 GAGTCTTCTCTCTTCAAGCCACTCTTCTTCTGATTTCTAGGAAACCGTAAAGTAAAGAC 717
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Db 718 AGGCCTTTCTTTTGGT 733
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RESULT 14
LOCUS AW266498 ZG24 gastric epithelial cell GES-1 Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION AW266498
VERSION AW266498.1 GI:6646676
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 330)

Db 604 CACTGTGTTTCATTTTCATACCCCTTTACTTTGTCCCTGGCAATGTTTCTCTCCATCTT 663
Qy 600 TTCTTTGTAAACATCTCAAGAGATGCAGCTCCCATGGTAAAGGAT 646
Db 664 CTCCATGTGGAAACATCGCAGAGATGCAGCACACTGTCTCAAAATAT 710

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Job time : 4558 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2006, 20:16:31 ; Search time 312 Seconds
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Title: US-09-825-882-7

Perfect score: 930

Sequence: 1 atgataacttttaccat.....agaagacttcattcccatag 930

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 9: /cgn2_6/ptodata/1/ina/RE/COMB.seq.*
- 10: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 684.4 | 73.6 | 903 | 3 | US-09-949-016-14724 |
| 3 | 536.6 | 57.7 | 601 | 3 | US-09-949-016-108237 |
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| 5 | 481.4 | 51.8 | 601 | 3 | US-09-949-016-108297 |
| 6 | 472.2 | 50.8 | 601 | 3 | US-09-949-016-108236 |
| 7 | 451.2 | 48.5 | 601 | 3 | US-09-949-016-108441 |
| 8 | 449.4 | 48.1 | 601 | 3 | US-09-949-016-108442 |
| 9 | 428.4 | 46.1 | 601 | 3 | US-09-949-016-108480 |
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| 11 | 406 | 43.7 | 601 | 3 | US-09-949-016-108440 |
| 12 | 404.4 | 43.5 | 601 | 3 | US-09-949-016-108327 |
| 13 | 398.6 | 42.9 | 601 | 3 | US-09-949-016-108134 |
| 14 | 379 | 40.8 | 601 | 3 | US-09-949-016-108139 |
| 15 | 368.8 | 39.7 | 601 | 3 | US-09-949-016-108443 |
| 16 | 347.6 | 37.4 | 601 | 3 | US-09-949-016-108273 |
| 17 | 345.6 | 37.2 | 601 | 3 | US-09-949-016-108326 |
| 18 | 340.8 | 36.6 | 954 | 3 | US-09-949-016-108440 |
| 19 | 336.8 | 36.2 | 554 | 3 | US-09-949-016-108327 |
| 20 | 331.2 | 35.6 | 601 | 3 | US-09-949-016-108438 |
| 21 | 308.2 | 33.1 | 912 | 3 | US-09-949-016-108438 |
| 22 | 295.6 | 31.8 | 601 | 3 | US-09-949-016-108481 |
| 23 | 293.6 | 31.6 | 397 | 3 | US-09-949-016-108481 |
| 24 | 288.2 | 31.0 | 391 | 3 | US-09-949-016-108349 |

RESULT 1

US-09-949-016-14724

; Sequence 14724, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14724

; LENGTH: 250352

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(250352)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14724

Query Match 89.0%; Score 827.6; DB 3; Length 250352;

Best Local Similarity 93.1%; Pred. No. 9e-226;

Matches 866; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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| Db | 122572 | ATGATAACTTTTCTGCCCATCATTTTTCATTTTCCATTAATAGTGGTACATTTGTTATTGGA 122631 |
| Qy | 61 | AATTTTCTAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAGAGACAAAAG 120 |
| Db | 1226..2 | AATTTTCTAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAGAGACAAAAG 122691 |
| Qy | 121 | ATCTCTTTGCTGACAAAATTCACGTCTGCGGTCTCCAGAGTTGGTTGCTCTGG 180 |
| Db | 1226..3 | ATCTCTTTGCTGACAAAATTCACGTCTGCGGTCTCCAGAGTTGGTTGCTCTGG 122751 |
| Qy | 181 | GTATTATATTAACCTGGTATTCACTGTGTTGAATCCAGCTTTTATAGTGTAGTAAGTA 240 |

ALIGNMENTS

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| | 26 | 284.4 | 30.6 | 466 | 3 | US-09-949-016-108371 | Sequence 71, Appl |
| c | 27 | 281.6 | 30.3 | 601 | 3 | US-09-949-016-108329 | Sequence 108329, |
| c | 28 | 277.4 | 29.8 | 601 | 3 | US-09-949-016-108366 | Sequence 108366, |
| c | 29 | 269.6 | 29.0 | 601 | 3 | US-09-949-016-108272 | Sequence 108272, |
| c | 30 | 241.2 | 25.9 | 601 | 3 | US-09-949-016-108367 | Sequence 108367, |
| | 31 | 226.4 | 24.3 | 2438 | 3 | US-09-949-016-15124 | Sequence 15124, A |
| | 32 | 220 | 23.7 | 954 | 3 | US-09-949-016-15124 | Sequence 15124, A |
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| | 38 | 186.8 | 20.1 | 1084 | 3 | US-09-949-016-15124 | Sequence 15124, A |
| | 39 | 181.8 | 19.5 | 1532 | 3 | US-09-949-016-15124 | Sequence 15124, A |
| | 40 | 179.6 | 19.3 | 601 | 3 | US-09-949-016-15124 | Sequence 15124, A |
| c | 41 | 178.6 | 19.2 | 1739 | 3 | US-09-949-016-15124 | Sequence 15124, A |
| | 42 | 175.4 | 18.9 | 1540 | 3 | US-09-949-016-15124 | Sequence 15124, A |
| | 43 | 172.4 | 18.5 | 951 | 3 | US-09-949-016-15124 | Sequence 15124, A |
| | 44 | 172.4 | 18.5 | 951 | 3 | US-09-949-016-15124 | Sequence 15124, A |
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Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTTGCAATTTCTCAACTTTTATTTTCTTCCAC 360
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Db 122992 GTTGTCTATTTTGTGATAAATGATGAGATTTGCGGACAAAAGAAATTTGAAGGA 123051
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Db 123052 AACATGACTTGAAGATCAAAATTTGAAGAGTGAATGTACTTTTCAAAATATGACTGTAAACC 123111
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Db 123112 ATCCTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGT 123171
Qy 601 TCTTTGTGTAACATCTCAAGAGATGAGCTTCCATGTTAAAGGATCTCAAGATCCCAGC 660
Db 123172 TCTCTGTGTAACATCTCAAGAGATGAGCTTCCATGTTAAAGGATCTCAAGATCCCAGC 123231
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Qy 721 TACTTTCTGTCATAATGATATCAGTTTGGAGTTTGGAGTCTGGAAAAACAACCTGTCTC 780
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Qy 841 TGGGAAAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGGCAATGAGTACTGG 900
Db 123412 TGGGAAAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGGCAATGAGTACTGG 123471
Qy 901 GTGAAAGGAGAGAGAGCTTCATCTCCATAG 930
Db 123472 GTGAAAGGAGAGAGAGCTTCATCTCCATAG 123501

RESULT 2

US-09-393-634-63

; Sequence 63, Application US/09393634

; Patent No. 6558910

; GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.

; APPLICANT: Adler, Jon Elliot

; APPLICANT: Ryba, Nick

; APPLICANT: Mueller, Ken

; APPLICANT: Hoon, Mark

; APPLICANT: The Regents of the University of California

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by the Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors

; FILE REFERENCE: 02307E-098000US

; CURRENT APPLICATION NUMBER: US/09/393,634

; CURRENT FILING DATE: 1999-09-10

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 63

; LENGTH: 903

; TYPE: D1/2
; ORGANISM: Homo sapiens
; FEATURE
; OTHER INFORMATION: human GR15
US-09-393-634-63

Query Match 73.6%; Score 684.4; DB 3; Length 903;

Best Local Similarity 85.7%; Pred. No. 7.4e-186;

Matches 773; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

Qy 1 ATGATAACTTTTTCACCCATCATTTTTCAGTCTGGTAGTGGTTTACATTTGTTTATGGA 60
Db 1 ATGATAACTTTTTCACCCATCATTTTTCAGTCTGGTAGTGGTTTACATTTGTTTATGGA 60
Qy 61 AATTTTGTCTAATGGCTTCATAGCACTGTAATTTCCATTTGAGTGGTTCAGAGACAAAAG 120
Db 61 AATTTTGTCTAATGGCTTCATAGTGTGGTAAATTTCCATTTGAGTGGTTCAGAGACAAAAG 120
Qy 121 ATCTCCTTTGTCTGACCAAAATTTCTCACTGCTCTGGGGTCTCCAGAGTTGGTTTGTCTGG 180
Db 121 ATCTCCTTTGTCTGACCAAAATTTCTCACTGCTCTGGCAGTCTCCAGAGTTGGTTTGTCTGG 180
Qy 181 GTATTATTATTAACCTGGTATTCAACTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 181 GTAATATTATTATGATTTGATGCAACTGTTTGAATCCAGGTTTATATAGTTAGAGTA 240
Qy 241 AGAATCTACTGCTTATAATATCTGGCAGTGTATCAACCAATTTTCAGCAACTGGCTTGTACT 300
Db 241 AGAATCTACTGCTTATAATGCTGGCTGTAAACCAACCAATTTTCAGCATCTGGGTTGTACT 300
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTTGCCAATTTTCTCAACTTTTATTTTCTTCCAC 360
Db 301 AGCCTCAGCATATTTTATTTTCTCAAGATTTGCCAATTTTCTCAACTTTTATTTTCTTCCAC 360
Qy 361 TTAAGAGAGAGAGTAAAGAGTGTCACTCTGGTGATGTTTGTGGGCTTTTGTCTATTTTG 420
Db 361 TTAAGAGAGAGAGTAAAGAGTGTCACTCCAGTGTACTATTGGGGCTTTTGTCTATTTTG 420
Qy 421 GCTTGTCTATCTTTTGTGATAAATGATGAGATTTGGCGGACAAAAGAAATTTCAAGGA 480
Db 421 GTTGTCTATCTTTTGTGATAAATGATGAGATTTGGCGGACAAAAGAAATTTCAAGGA 480
Qy 481 AACATGACTTGGAAAGATCAAAATTTGAAGAGTGTCAATGTACTTTTCAAAATATGACTGTAAACC 540
Db 481 AACGTGAGTGGGAGATCAAAATTTGAGTGTATCCGACGACCTTTTCAGATATGACTGTAAACC 540
Qy 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTAAATCTGT 600
Db 541 ACGCTTGCAAAACCTTAAATACCCCTTTACTCTGCTCCCTGTTTATCTTTTCTGCTTAAATCTGT 600
Qy 601 TCTTTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCAAGATCCCAGC 660
Db 601 TCTTTGTGTAACATCTCAAGAGATGAGCTCCATGTTAAAGGATCTCCAGATTTCCAAAC 660
Qy 661 ACCAAGGTCCACATAAAGAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCCATT 720
Db 661 ACCAAGGTCCACATAAAGAGCTTTGCAAACTGTGATCTCCTCTCTTGTATGTGCCATT 720
Qy 721 TACTTTCTGTCATAATGATATCAGTTTGGAGTTTTT---GGAAGTCTGGAACAAAACCT 777
Db 721 TACTTTCTGTCATAATGATATCAGATTTTGGAAATTTTAGGAGGAGGCTGTAGAACAACCT 780
Qy 778 GCTTCTAGTCTGCAAGCTATTAGATTCAGCTATCTTCAATCCACCCATTTCATCTCTG 837
Db 781 GTCTCATGCTCAGCCAAACTACTGCAATATATATACCTTCTATTTCATTCATTCCTTA 840
Qy 838 ATTTGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGGCAATAGAGGTAC 897
Db 841 ATTTGGGGAACAAGAGCTAAAGCAGACTTTTCTTTCAGTTTGTGGCAATAGAGGTAC 897
Qy 898 TG 899
Db 901 TG 902

Db 1 C 1

RESULT 5

US-09-949-016-108297/c
; Sequence 108297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108297
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-108297

Query Match 51.8%; Score 481.4; DB 3; Length 601;
Best Local Similarity 92.2%; Pred. No. 8.5e-128;
Matches 506; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 382 GTCATTCGTGATGTTGTGGGCTTTTGCTATTTTGGCTGTGCATCTTTTGTGATA 441
Db |||||
601 GTTGTTCTGGTGATACTATGGGCTTTGCTATTTTGGTTGTGATCTTTTGTGATA 542
QY 442 AACATGATGAGATTGTCGGNCAAAAGATTGGAAGAAACATGACTTGGAGATCAA 501
Db |||||
541 AACATGAATCAGATTATATGGAACAAAGAAATATGAAGGAAACATGACTTGGAGATCAA 482
QY 502 TTGAAGAGTGCAATCTACTTTTCAATATGACTGTAAACCATGGTAGCAAACTTAGTACC 561
Db |||||
481 CTGAGAGTGCAATGATCCTTTCAATACACGGTAAACATCTAGCAAACTTAGTACC 422
QY 562 TTCACCTGACCTACTATCTTTTATGCTGTGTAATCTGTTCTTTGTGTAACATCTCAAG 621
Db |||||
421 TTCACCTGACCTGATATCTTTCTGCTGTTAAATCTGTTCTGTTAAACATCTCAAA 362
QY 622 AGATGCGAGCTCCATGGTAAAGGATCTCAAGATCCAGACCAAGGTCACATAAAGCT 681
Db |||||
361 AAGATGCGAGCTCCATGGCAAGGATCTCAAGATCCAGATCCAGATCCAGATCCAGATCC 302
QY 682 TTGCAAACTGATCTCTCTCTCTGTTATGTCGCAATTTACTTTCTGTCATATGATA 741
Db |||||
301 WTGCAAACTGATCTCTCTCTCTGTTATGTCGCAATTTACTTTCTGTCATATCATG 242
QY 742 TCAGTTTGGAGTTTGGAGTCTGGAAGCTGGAACCAAACTGCTTCATGTTCTGCAAGCTATT 801
Db |||||
241 TCAGTTTGGAGTTTGGAGTCTGGAAGCTGGAACCAAACTGCTTCATGTTCTGCGAAGCTATT 182
QY 802 AGATTTCAGTATCTCTCAATCACCCTTCAATCTGATTTGGGAAACCAAGAGCTAAAG 861
Db |||||
181 GCAATTCAGTATCTCTCAATCACCCTTCAATCTGATTTGGGAAACCAAGAGCTAAAG 122
QY 862 CAGACTTTTCTTTCAGTTTGGGCAAAATGAGGTACTGGGTGAAAGGAGAGAGACTTCA 921
Db |||||
121 CAGACTTTTCTTTCAGTTTGGGCAATGATGAGGTACTGGGTGAAAGGAGAGAGACTTCA 62
QY 922 TCTCCATAG 930
Db |||||
61 TCTTCATAG 53

RESULT 6

US-09-949-016-108236/c
; Sequence 108236, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108236
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-108236

Query Match 50.8%; Score 472.2; DB 3; Length 601;
Best Local Similarity 93.4%; Pred. No. 3.7e-125;
Matches 492; Conservative 1; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTACCCCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db |||||
527 ATGATAACTTTTCCCCCATCATTTTCCATTTAGTAGTGGTTACATTTGTTATTGGA 468
QY 61 AATTGTTGTAATGGCTTCATAGCACTGGTAAATTCATTTAGTGGTTCAAGAGACAAAAG 120
Db |||||
467 AATTGTTGTAATGGCTTCATAGCGTTGGTAAATTCACCGAGTGGTGAAGAGACAAAAG 408
QY 121 ATCTCCTTTGCTGACCAAAATTCATCTCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||
407 ATCTCCTTTGCTGACCAAAATTTGTCACCTCTCTGGGGTCTCCAGAGTTGGTTGCTCTGG 348
QY 181 GTATTATTATTAATCGTGTATTTCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db |||||
347 GTGTTATTATTAATTTGGTATTTCACTGTGTTGAATCCAGCTTTTTRTAGTGTAGAATA 288
QY 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTTGAGCAACTGGCTTGTCTACT 300
Db |||||
287 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCGGCCATTTTCAGCAACTGGGCTGTCTACT 228
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCTCAC 360
Db |||||
227 AGCTTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCCAACTTTATTTTCTTCTGCG 168
QY 361 TTAAGAGAGAGATTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTTGTATTTTGG 420
Db |||||
167 TTAAGAGAGAGATTAAAGAGTGTCAATCTGGTGATGTTGTTGGGCGCTTTTGTATTTTGG 108
QY 421 GCTTGTCATCTTTTGTGATATAAATGAATGAGATTTGCGGACAAAAGAAATTTGAGGA 480
Db |||||
107 GCTTGTCATCTTTTGTGTTAAACATGAATCAGATTTGATGACAAAAGAAATATGAGGA 48
QY 481 AACATGACTTGGAGATCAAAATTTGAAGAGTGAATGTACTTTTCTTCTTCTTCTTCTTCTT 527
Db |||||
47 AACATGACTTGGAGATCAAAATTTGAGGCGTGCATTTGCTTCTTCTTCTTCTTCTTCTTCT 1

RESULT 7

US-09-949-016-108441/c
; Sequence 108441, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108441
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108441

Query Match      48.5%; Score 451.2; DB 3; Length 601;
Best Local Similarity 84.5%; Pred. No. 3.8e-119;
Matches 507; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 130 GCTGACCAAAATCTCACTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGGGTATTATTA 189
DB 600 GCTGATCAAAATTAATGCTGCTCTGGAGTCTCCAGAGTTGGTTGCTCTGGGTAAATATTA 541

QY 190 TTAACCTGATTAATCACTGCTGCTGGGGTCTCCAGAGTTGGTTGCTCTGGGTATTATTA 249
DB 540 TTACATGATTAATCACTGCTGCTGGAGTCTCCAGAGTTGGTTGCTCTGGGTAAATATTA 481

QY 250 GCTTATAATATCTGGGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCT 309
DB 480 ATTCTTAATGCTGGGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCT 421

QY 310 ATATTTATTTGCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369
DB 420 ATATTTATTTGCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361

QY 370 AGAGTTAGAGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
DB 360 AAGGCTAAGAGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301

QY 430 CTTTGTGTATAAATGAATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
DB 300 CTTGTGTATAAATGAATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241

QY 490 TGAAGATCAAAATGAAGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCT 549
DB 240 TGAAGATCAAAATGAAGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCT 181

QY 550 AACTTAGTACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 609
DB 180 AACTTAGTACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121

QY 610 AAACATCTCAAGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
DB 120 AAACATCTCAAGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61

QY 670 CACATAAAAGCTTTTCAAGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCT 729
DB 60 CACATAAAAGCTTTTCAAGAGTGTATCAACCAATTTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCT 1
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RESULT 8
US-09-949-016-108442/c
; Sequence 108442, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108442
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108442

Query Match      48.3%; Score 449.4; DB 3; Length 601;
Best Local Similarity 84.4%; Pred. No. 1.2e-118;
Matches 504; Conservative 1; Mismatches 92; Indels 0; Gaps 0;

QY 146 CTGCTCTGGGGTCTCCAGAGTTGGTTGCTCTGGGTATTATTAATTAACCTGTTATCAA 205
DB 597 CTGCTCTGGGAGTCTCCAGAGTTGGTTGCTCTGGGTAAATATTAATTAACCTGTTATCAA 538

QY 206 CTGCTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACTGCTTATAATATCTGGG 265
DB 537 CTGCTGTTGAATCCAACTTCAATCAATTTTAAAGTAATAATTTTATTTCTAATGCCCTGGG 478

QY 266 CAGTGATCAACCAATTTTCAAGAGTGTAGAAGTAAGAACTACTGCTTATAATATCTGGTCA 325
DB 477 CAGTAACCAATCAATTTTCAAGAGTGTAGAAGTAAGAACTACTGCTTATAATATCTGGTCA 418

QY 326 AGATTGCCAATTTTCAAGAGTGTAGAAGTAAGAACTACTGCTTATAATATCTGGTCA 385
DB 417 AGATTGCCAATTTTCAAGAGTGTAGAAGTAAGAACTACTGCTTATAATATCTGGTCA 358

QY 386 TTCTGTGATGTTGTTGGGGCTTTGCTGATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445
DB 357 TTCTGTGATGTTGTTGGGGCTTTGCTGATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298

QY 446 TGAATGAGATGTTGCGGACAAAGAAATTTGAAGGAAACATGACTTGAAGAACTCAAAATGA 505
DB 297 CGTATATAATGTTGCGGACAAAGAAATTTGAAGGAAACATGACTTGAAGAACTCAAAATGA 238

QY 506 AGAGTCAATGTACTTTTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
DB 237 GGAATCAATGACCTTTTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 178

QY 566 CTCTGACCTTACTATCTTTTATGCTGTTAATCTGTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 625
DB 177 CTCTGACCTTACTATCTTTTATGCTGTTAATCTGTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 118

QY 626 TGAGCTCAATGTTAAGGATCTCAAGATCCAGACCAAGTCCCAAGTCCCAAGTCCCAAGTCCCAAGTCC 685
DB 117 TGAGCTCAATGTTAAGGATCTCAAGATCCAGACCAAGTCCCAAGTCCCAAGTCCCAAGTCCCAAGTCC 58

QY 686 AAACCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 742
DB 57 AAACCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1
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RESULT 9
US-09-949-016-108480/c
; Sequence 108480, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 108480
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108480

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| | | | | |
|-----------------------|----------------|--|----------|------------|
| Query Match | 45.1% | Score 428.4 | DB 3 | Length 601 |
| Best Local Similarity | 82.0% | Pred. No. 1.3e-112 | | |
| Matches 492 | Conservative 1 | Mismatches 107 | Indels 0 | Gaps 0 |
| Qy | 308 | GCATATTTTATTTTGCTCAAGATTGCCAAATTTCTCAAACCTTTATATTTTCTTCACTTAAAGA | 367 | |
| Db | 601 | GCATATTTTATTTTGCTCAAGATTGCCAAATTTCTCAAACCTTTCTTTTTCATTTTAAAGA | 542 | |
| Qy | 368 | GGAGAGTTAAGAGTGCATTTCTGTGTGATGTTGTTGGGCCCTTTCCTCATTTTTTGGCTTGTC | 427 | |
| Db | 541 | GGAGAGTTAGAGTGTCAATTCGTGTGATACGTGTTGGGACCTTCATATTTTTTGGTTTGTCTC | 482 | |
| Qy | 428 | ATCTTTTGTGATAAACATGAATCAGATATGTCGGCAGAAAGAAATTTGAAAGGAACATGA | 487 | |
| Db | 481 | ATCTTCTTGTGGCAACATGGAATGAGAGTATGTGGGCAGAAAGAAATATGAAGGAACATGA | 422 | |
| Qy | 488 | CTTGGAAAGTCAAATTCGAAGAGTGCATGTACTTTTCAAATATACACTGTAAACCATGGTAG | 547 | |
| Db | 421 | CTGGAGATGNAATTGAGGNATACAGTACATCTTTCATATTTGACTGTAACTACCCCTAT | 362 | |
| Qy | 548 | CAAACTTTAGTACCCCTTCACCTGTGACCCCTAATACTTTTTTATGCTGTTTAATCTGTTCTTTGT | 607 | |
| Db | 361 | GGAGCTTTCATACCCCTTTACTCTGTCCCTGATATCTTTTCTGATGCTAATCTGTTTCTCTGT | 302 | |
| Qy | 608 | GTAACATCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCCAAGACCAACGAAG | 667 | |
| Db | 301 | RTAAACATCTCAAGAAGATGCAGCTCCATGAGAGAGGATCCCAAGATCTCAGACCAACGAAG | 242 | |
| Qy | 668 | TCCACATAAAGCTTTGCCAACTGTGATCTCCTTCTTGTATTATGTCCTATTTACTTTTC | 727 | |
| Db | 241 | TCCACATAAAGCTTTGCCAACTCTGATCTCCTTCTTGTATTATGTCCTATTTTCTTTTC | 182 | |
| Qy | 728 | TGTCCTAATATCATAGTTTGGAGTTTGGAGTCTTGAAAAACAAACCTGTCTTCATGT | 787 | |
| Db | 181 | TATTCCTTAATCGTTTCGGTTTGGAGTCTTAGAGGCTTCGGAATGACCCCGGTGTCATGG | 122 | |
| Qy | 788 | TCTGCAAGCTATTAGATTACGTATCTCTCAATCCCAACCTTCATCTCTGATTTGGGAA | 847 | |
| Db | 121 | TTAGCAGGCTGTTGGAAAAATATATCTTGGATTCGACTCATTCATCTTAATTTGGAGAA | 62 | |
| Qy | 848 | ACAAGAAGCTAAAGCAGACTTTTCTTTGAGTTTTTTTGGCAAAATGAGGTACTGGGTGAAAG | 907 | |
| Db | 61 | CCAAAGAGCTAAAAACAACCTTTCTTTTGTATTTGTGTCAATTAGGTCGTGAGTAAAG | 2 | |

RESULT 10
 US-09-949-016-108328/c
 ; Sequence 108328, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03

| | |
|----|--|
| | ; PRIOR APPLICATION NUMBER: 60/231,498 |
| | ; PRIOR FILING DATE: 2000-09-08 |
| | ; NUMBER OF SEQ ID NOS: 207012 |
| | ; SOFTWARE: FastSeq for Windows Version 4.0 |
| | ; SEQ ID NO 108328 |
| | ; LENGTH: 601 |
| | ; TYPE: DNA |
| | ; ORGANISM: Human |
| | US-09-949-016-108328 |
| | |
| | Query Match 45.6%; Score 424. |
| | Best Local Similarity 82.7%; Pred. NO.: 1 |
| | Matches 496; Conservative 1; Mismatch |
| Qy | 145 ACTGCTCTGGCGGTCTCCAGAGTTCGGTTGG |
| Dd | 601 ACTCCTCTGGGTGTGCAGAATTTGGTTTTA |
| Qy | 205 ACTGTGTTGAATCCACAGCTTTTAAATAGTCTAATA |
| Dd | 541 ACTGTGTTAAATTTGGCTTCATATAGATTATTA |
| Qy | 265 GCAGTGATCAACCAATTTTCAGCAA CTGGCTTT |
| Dd | 481 GCAATAACCAAGCATTTTCAGCATCTGG-GT |
| Qy | 325 AAGATTTGCCAAATTTCTCCAAC TTTTATTTTTT |
| Dd | 422 AAGACTGCCAATTTCTCCAACTTTATTTTTT |
| Qy | 385 ATTCGTGTGATGTGTTGGGGCCCTTTTGGCTA |
| Dd | 362 GTTTTGGTGATGCTGTTGGGGCCCTTTGGTA |
| Qy | 445 ATGAATGAGATGTGCGGACAAAAGAAATTTT |
| Dd | 302 AYGGTGAGAGTGTGTGGACAAAAGAAATAT |
| Qy | 505 AAGAGTGCAAATGTACTTTTCAAAATATGACTT |
| Dd | 242 AGGAATGCAATACAGCTTTCAAAC TTGACT |
| Qy | 565 ACTCTGACCCTACTATCTTTTATGCTGTATA |
| Dd | 182 ACTCTGACCTAAATATCTTTTCTGCTGTATA |
| Qy | 625 ATGCAGCTCCATGGTAAAGGATCTCAAGAT |
| Dd | 122 ATGCAGCTCCATGGCAAGGATCTCAACAT |
| Qy | 685 CAAACTGTGATCTCTTCCCTCTTGTTATGTG |
| Dd | 62 CAAACTGTGATCTCTTCCCTTATGTTATTTT |
| | RESULT 11 |
| | US-09-949-016-108440/c |
| | ; Sequence 108440, Application US/09949016 |
| | ; Patent No. 6812339 |
| | ; GENERAL INFORMATION: |
| | ; APPLICANT: VENTER, J. Craig et al. |
| | ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN |
| | ; FILE REFERENCE: CL001307 |
| | ; CURRENT APPLICATION NUMBER: US/09/949,016 |
| | ; CURRENT FILING DATE: 2000-04-14 |
| | ; PRIOR APPLICATION NUMBER: 60/241,755 |
| | ; PRIOR FILING DATE: 2000-10-20 |
| | ; PRIOR APPLICATION NUMBER: 60/237,768 |
| | ; PRIOR FILING DATE: 2000-10-03 |
| | ; PRIOR APPLICATION NUMBER: 60/231,498 |
| | ; PRIOR FILING DATE: 2000-09-08 |
| | ; NUMBER OF SEQ ID NOS: 207012 |

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RESULT 11
US-09-349-016-108440/c
; Sequence 108440, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/349,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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||||| 420 TGCTGTTAATCTACTCTCTGTGTAAACAATCTGAAGAGATGAGCTCCATGGCAAAGGAT 361
Qy 647 CTCAGATCCAGCACCAAGGTCCACATAAAGCTTTGCAAACTGTGATCTCCTTCTCT 706
Db 360 CTCAGATCCAGCACCAAGATCCACATAAAGCTCTGCAAACTGTGACCTCCTTCTCT 301
Qy 707 TGTATGTGCCATTACTTTCTGTCCATAATGATATCAGTTTGGAGTTTGGAAAGTCTGG 766
Db 300 TATTACTTGGCAATTTACTTTCTGTCTTAATCATATCGTTTGGAAATTTAAGATGCTAC 241
Qy 767 AARACAAACCTGTCTCATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACC 826
Db 240 CAAAAGAAATGTCTTAATGCTTTGCCAAGCTTTTGGAAATCATATATCCATCTCCACT 181
Qy 827 CATTCATCTGATTTGGGGAACAAGAGCTAAAGCAGACTTTTCTTTTCAAGTTTGTGGC 886
Db 180 CATTCATCTGATTTGGGGAACAAGAGCTAAAGCAGACCTTTCTTTTCAAGTTTGTGGC 121
Qy 887 AATGAGGTACTGGGTGAAGGAGAGAGACTTCATCTCCATAG 930
Db 120 AGGTGACTTGTGGGCAAAAGGACAGAACCAAGTCAACTCCATAG 77
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Search completed: April 29, 2006, 20:21:52
Job time : 314 secs

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GenCore version 5.1.7
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QM nucleic - nucleic search, using sw model

Run on: May 1, 2006, 07:22:47 ; Search time 846 Seconds
(without alignments)
9090.451 Million cell updates/sec

Title: US-09-825-882-7

Perfect score: 930

Sequence: 1 atgataactttttaccat.....agaagacttcatctccatag 930

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA Main:*
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 - 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 930 | 100.0 | 930 | 3 | US-09-825-882-7 |
| 2 | 930 | 100.0 | 930 | 6 | US-10-191-058-6 |
| 3 | 930 | 100.0 | 930 | 7 | US-10-343-650A-681 |
| 4 | 930 | 100.0 | 930 | 8 | US-10-724-208-7 |
| 5 | 930 | 100.0 | 930 | 8 | US-10-770-127-178 |
| 6 | 930 | 100.0 | 930 | 8 | US-10-724-209-7 |
| 7 | 930 | 100.0 | 930 | 9 | US-10-986-871-7 |
| 8 | 930 | 100.0 | 1330 | 6 | US-10-017-161-1835 |
| 9 | 930 | 100.0 | 1330 | 6 | US-10-292-798-1491 |
| 10 | 851.6 | 91.6 | 930 | 3 | US-09-825-882-11 |
| 11 | 851.6 | 91.6 | 930 | 7 | US-10-343-650A-691 |
| 12 | 851.6 | 91.6 | 930 | 8 | US-10-724-208-11 |
| 13 | 851.6 | 91.6 | 930 | 8 | US-10-770-127-182 |
| 14 | 851.6 | 91.6 | 930 | 8 | US-10-724-209-11 |
| 15 | 851.6 | 91.6 | 930 | 9 | US-10-986-871-11 |
| 16 | 851.6 | 91.6 | 971 | 5 | US-10-219-834-5 |
| 17 | 851.6 | 91.6 | 1330 | 6 | US-10-017-161-1837 |
| 18 | 851.6 | 91.6 | 1330 | 6 | US-10-292-798-1493 |
| 19 | 829.2 | 89.2 | 930 | 3 | US-09-825-882-19 |
| 20 | 829.2 | 89.2 | 930 | 8 | US-10-724-208-19 |
| 21 | 829.2 | 89.2 | 930 | 8 | US-10-770-127-190 |
| 22 | 829.2 | 89.2 | 930 | 8 | US-10-724-209-19 |
| 23 | 829.2 | 89.2 | 930 | 9 | US-10-986-871-19 |

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|----|-------|------|------|---|--------------------|-------------------|
| 24 | 829.2 | 89.2 | 1330 | 6 | US-10-017-161-1931 | Sequence 1931, Ap |
| 25 | 829.2 | 89.2 | 1330 | 6 | US-10-292-798-1583 | Sequence 1583, Ap |
| 26 | 829.2 | 88.5 | 1300 | 6 | US-10-292-798-1479 | Sequence 1479, Ap |
| 27 | 819.6 | 88.1 | 1300 | 6 | US-10-017-161-1823 | Sequence 1823, Ap |
| 28 | 799.6 | 86.0 | 1360 | 6 | US-10-017-161-1825 | Sequence 1825, Ap |
| 29 | 799.6 | 86.0 | 1360 | 6 | US-10-292-798-1481 | Sequence 1481, Ap |
| 30 | 796.4 | 85.6 | 960 | 6 | US-10-191-058-4 | Sequence 4, Appl |
| 31 | 796.4 | 85.6 | 960 | 6 | US-10-343-650A-667 | Sequence 667, App |
| 32 | 795 | 85.5 | 900 | 7 | US-10-343-650A-669 | Sequence 669, App |
| 33 | 773.2 | 83.1 | 930 | 3 | US-09-510-332-57 | Sequence 57, Appl |
| 34 | 773.2 | 83.1 | 930 | 8 | US-10-770-127-57 | Sequence 57, Appl |
| 35 | 773.2 | 83.1 | 930 | 9 | US-10-962-365-57 | Sequence 57, Appl |
| 36 | 751.6 | 80.8 | 960 | 3 | US-09-510-332-52 | Sequence 52, Appl |
| 37 | 751.6 | 80.8 | 960 | 8 | US-10-770-127-52 | Sequence 52, Appl |
| 38 | 751.6 | 80.8 | 960 | 9 | US-10-962-365-52 | Sequence 52, Appl |
| 39 | 751.4 | 80.8 | 900 | 3 | US-09-510-332-54 | Sequence 54, Appl |
| 40 | 751.4 | 80.8 | 900 | 8 | US-10-770-127-54 | Sequence 54, Appl |
| 41 | 751.4 | 80.8 | 900 | 9 | US-10-962-365-54 | Sequence 54, Appl |
| 42 | 741.2 | 79.7 | 930 | 3 | US-09-510-332-61 | Sequence 61, Appl |
| 43 | 741.2 | 79.7 | 930 | 8 | US-10-770-127-61 | Sequence 61, Appl |
| 44 | 741.2 | 79.7 | 930 | 9 | US-10-962-365-61 | Sequence 61, Appl |
| 45 | 735.8 | 79.1 | 930 | 3 | US-09-510-332-63 | Sequence 63, Appl |

ALIGNMENTS

RESULT 1

US-09-825-882-7
; Sequence 7, Application US/09825882
; Patent No. US20020094551A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/09/825,882
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-882-7

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|-----------------------|-----------------|--|-----------|-------------|
| Query Match | 100.0% | Score 930; | DB 3; | Length 930; |
| Best Local Similarity | 100.0%; | Pred. No. 1.8e-245; | | |
| Matches 930; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | ATGATAACTTTTCTACCCATCATTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA | 60 | |
| Db | 1 | ATGATAACTTTTCTACCCATCATTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA | 60 | |
| Qy | 61 | AATTTTCTAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGACAGACAAAAG | 120 | |
| Db | 61 | AATTTTCTAATGGCTTCATAGCACTGTAATTCATTTGAGTGGTTCAAGACAGACAAAAG | 120 | |
| Qy | 121 | ATCTCCTTTGCTGACCAAAATTCACCTGCTCTGCGGCTCTCCAGAGTTGGTTGCTCTGG | 180 | |
| Db | 121 | ATCTCCTTTGCTGACCAAAATTCACCTGCTCTGCGGCTCTCCAGAGTTGGTTGCTCTGG | 180 | |
| Qy | 181 | GTATTATTATAACTGGTATTCACTGTTGATCCAGCTTTTATAGTGTAGAGTA | 240 | |
| Db | 181 | GTATTATTATAACTGGTATTCACTGTTGATCCAGCTTTTATAGTGTAGAGTA | 240 | |
| Qy | 241 | AGAACTACTGCTTATATATATCTGGGAGTGTATCAACCAATTCAGCAACTGGCTGCTACT | 300 | |
| Db | 241 | AGAACTACTGCTTATATATATCTGGGAGTGTATCAACCAATTCAGCAACTGGCTGCTACT | 300 | |


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; Sequence 681, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 681
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-10-343-650A-681

Query Match
Best Local Similarity 100.0%; Score 930; DB 7; Length 930;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAACTTTTCTACCCATCATTTTCCAGTCTGGTAGTGTATACATTTGTTATTGGA 60
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QY 61 AATTTTGTAAATGGCTTCATAGACATCGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120
DB 61 AATTTTGTAAATGGCTTCATAGACATCGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120
QY 121 ATCTCTTTGTGACCAAAATCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
DB 121 ATCTCTTTGTGACCAAAATCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
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DB 241 AGAATCTGCTTATTAATATCTGGGAGTGTATCAACCATTTTCCAGCAACTGGCTTGTACT 300
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTTGCCAATTTCTCCAACTTTATTTTCTTCC 360
DB 301 ACCCTCAGCATATTTTATTTGCTCAAGATTTGCCAATTTCTCCAACTTTATTTTCTTCC 360
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; Sequence 681, Application US/10724208
; Publication No. US20040209313A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/724,208
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-208-7

Query Match
Best Local Similarity 100.0%; Score 930; DB 8; Length 930;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AATTTTGTAAATGGCTTCATAGACATCGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120
DB 61 AATTTTGTAAATGGCTTCATAGACATCGGTAAATTCATTGAGTGGTTCAAGAGACAAAAG 120
QY 121 ATCTCTTTGTGACCAAAATCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
DB 121 ATCTCTTTGTGACCAAAATCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
QY 181 GTATTATTATAAATCTGGTAAATCCAGCTTTTAAATAGTGTAGAAGTA 240
DB 181 GTATTATTATAAATCTGGTAAATCCAGCTTTTAAATAGTGTAGAAGTA 240
QY 241 AGAATCTGCTTATTAATATCTGGGAGTGTATCAACCATTTTCCAGCAACTGGCTTGTACT 300
DB 241 AGAATCTGCTTATTAATATCTGGGAGTGTATCAACCATTTTCCAGCAACTGGCTTGTACT 300
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTTGCCAATTTCTCCAACTTTATTTTCTTCC 360
DB 301 ACCCTCAGCATATTTTATTTGCTCAAGATTTGCCAATTTCTCCAACTTTATTTTCTTCC 360
QY 361 TTAAGAGAGAGAGTTAAGAGTGTCAATTCGTGTGATTTGTTGGGCGCTTTTGTCTATTTTG 420
DB 361 TTAAGAGAGAGAGTTAAGAGTGTCAATTCGTGTGATTTGTTGGGCGCTTTTGTCTATTTTG 420
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QY 421 GCTTGTCACTTTTGTGATAAATCATGAATGAGATTCTGCGGACAAAGAAATTTGAAGGA 480
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QY 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGAATGACTTTTCAAAATATGACTGTAACC 540
Db 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGAATGACTTTTCAAAATATGACTGTAACC 540
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTGACCTGATCTCTTCTCTTCTTCTTCTTCTTCT 600
Db 541 ATGGTAGCAAACTTAGTACCCCTTCACTGACCTGATCTCTTCTCTTCTTCTTCTTCTTCT 600
QY 601 TCTTTGTGTAACATCTCAAGAGATGAGTCCATGCTGTAAGAGTCTCAAGATCCCGAGC 660
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QY 661 ACCAAGTCCACATAAAGCTTTGCAAACTGTGATCTCTTCTCTTCTTCTTCTTCTTCTTCT 720
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QY 781 TTCAATGTTCTGCAAGCTATTAGATTGAGTCTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
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QY 841 TGGGAAACAAAGAGCTTTAAAGCAGACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
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RESULT 5

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; Sequence 178, Application US/10770127
; Publication No. US20040214239A1
; GENERAL INFORMATION:
; APPLICANT: SERVANT, GUY
; APPLICANT: OZEK, MARK
; APPLICANT: BRUST, PAUL
; APPLICANT: XU, HONG
; TITLE OF INVENTION: FUNCTIONAL COUPLING OF T1RS AND T2RS BY GI PROTEINS
; TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF T1R
; TITLE OF INVENTION: AND T2R MODULATORS
; FILE REFERENCE: 100337.54281US
; CURRENT APPLICATION NUMBER: US/10/770,127
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/444,172
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/457,318
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-127-178
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Best Local Similarity 100.0%; Pred. No. 1.8e-245;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATACCTTTTACCCATCATTTTTCAGTCTGCTAGTGGTACATTTGTTATTTGGA 60
Db 1 ATGATAAATCTTTTACCCATCATTTTTCAGTCTGCTAGTGGTACATTTGTTATTTGGA 60
QY 61 AATTTTCTAATGCTTTCATAGCAGCTGGTAAATTCATTTGAGTGGTTCAGAGACAAAAG 120
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QY 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTGCGGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTGCGGGTCTCCAGAGTTGGTTGCTCTGG 180
QY 181 GTATTATTATTAACTCGTATTCACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAATA 240
Db 181 GTATTATTATTAACTCGTATTCACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAATA 240
QY 241 AGAACTACTGCTTATAATATCTGGGCGAGTGAATCAACCAATTTTCAGCAACTGGCTCTACT 300
Db 241 AGAACTACTGCTTATAATATCTGGGCGAGTGAATCAACCAATTTTCAGCAACTGGCTCTACT 300
QY 301 ACCCTCAGCATATTTTATTTTGTCTCAAGATTGCCAAATTTCTCAAATTTTCTTCTTCTCAC 360
Db 301 ACCCTCAGCATATTTTATTTTGTCTCAAGATTGCCAAATTTCTCAAATTTTCTTCTTCTCAC 360
QY 361 TTAAGAGGAGAGTAAAGAGTGTCACTTCTGTTGATGTTGTTGGGCGCTTTTCTGCTATTTTGT 420
Db 361 TTAAGAGGAGAGTAAAGAGTGTCACTTCTGTTGATGTTGTTGGGCGCTTTTCTGCTATTTTGT 420
QY 421 GCTTGTCACTTTTGTGATAAATCATGAATGAGATTGTGCGGACAAAGAAATTTGAAGGA 480
Db 421 GCTTGTCACTTTTGTGATAAATCATGAATGAGATTGTGCGGACAAAGAAATTTGAAGGA 480
QY 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGAATGACTTTTCAAAATATGACTGTAACC 540
Db 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGAATGACTTTTCAAAATATGACTGTAACC 540
QY 541 ATGTTAGCAAACTTAGTACCCCTTCACTGACCTGATCTCTTCTTCTTCTGTTTAACTGTT 600
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QY 661 ACCAAGTCCACATAAAGCTTTGCAAACTGTGATCTCTTCTCTTCTTCTTCTTCTTCTTCT 720
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QY 721 TACTTCTGTCATAATGATATCAAGTGTGAGTTTGGAGTCTGGAAGTCTGGAACCAACCTGTC 780
Db 721 TACTTCTGTCATAATGATATCAAGTGTGAGTTTGGAGTCTGGAAGTCTGGAACCAACCTGTC 780
QY 781 TTCAATGTTCTGCAAGCTATTAGATTGAGTCTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
Db 781 TTCAATGTTCTGCAAGCTATTAGATTGAGTCTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
QY 841 TGGGAAACAAAGAGCTTTAAAGCAGACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 841 TGGGAAACAAAGAGCTTTAAAGCAGACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
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Db 901 GTGAAGGAGAGAGAGCTTCAATCTCCATAG 930
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RESULT 6

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US-10-724-209-7
; Sequence 7, Application US/10724209
; Publication No. US20040248149A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 100337.54075US
; CURRENT APPLICATION NUMBER: US/10/724,209
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
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;; PRIOR FILING DATE: 2000-11-13
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 7
;; LENGTH: 930
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-724-209-7

Query Match 100.0%; Score 930; DB 8; Length 930;
Best Local Similarity 100.0%; Pred. No. 1.8e-245;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATAACTTTTCCACCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db |||||
Qy 1 ATGATAACTTTTCCACCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db |||||

Qy 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGCAAAAG 120
Db |||||

Qy 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGCAAAAG 120
Db |||||

Qy 121 ATCTCTCTTCTGCAACCAATTTCTCAGTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||

Qy 121 ATCTCTCTTCTGCAACCAATTTCTCAGTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||

Qy 181 GTATTATTATTAACCTGGTATTCACACTGTGTGAATCCAGCTTTTAAATAGTGTAAGTA 240
Db |||||

Qy 181 GTATTATTATTAACCTGGTATTCACACTGTGTGAATCCAGCTTTTAAATAGTGTAAGTA 240
Db |||||

Qy 241 AGAAGTCTCTTATATATCTGGGCGAGTATCAACCATTTCCAGCACTGGCTTGCTACT 300
Db |||||

Qy 241 AGAAGTCTCTTATATATCTGGGCGAGTATCAACCATTTCCAGCACTGGCTTGCTACT 300
Db |||||

Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCCAATTTTATTTTCTTAC 360
Db |||||

Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCCAATTTTATTTTCTTAC 360
Db |||||

Qy 361 TTTAAAGAGGAGGTTAAGAGTGTCAATTCGATGTGTGTTGGGGCCCTTTGCTATTTTGG 420
Db |||||

Qy 361 TTTAAAGAGGAGGTTAAGAGTGTCAATTCGATGTGTGTTGGGGCCCTTTGCTATTTTGG 420
Db |||||

Qy 721 TACTTTCTGTCAT 780
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Qy 721 TACTTTCTGTCAT 780
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Qy 781 TTCTGTTCTGCAAGCTAT 840
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Qy 781 TTCTGTTCTGCAAGCTAT 840
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Qy 841 TGGGGAAACAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCT 900
Db |||||

Qy 841 TGGGGAAACAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCT 900
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Db |||||

Qy 901 GTGAAGAGGAGAGAGACTTTCATCTCCATAG 930
Db |||||

RESULT 7
US-10-986-871-7
; Sequence 7, Application US/10986871
; Publication No. US2005006944A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/10/986,871
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/825,882
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-986-871-7

Query Match 100.0%; Score 930; DB 9; Length 930;
Best Local Similarity 100.0%; Pred. No. 1.8e-245;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATAACTTTTCCACCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db |||||

Qy 1 ATGATAACTTTTCCACCATCATTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db |||||

Qy 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGCAAAAG 120
Db |||||

Qy 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGCAAAAG 120
Db |||||

Qy 121 ATCTCTCTTCTGCAACCAATTTCTCAGTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||

Qy 121 ATCTCTCTTCTGCAACCAATTTCTCAGTCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db |||||

Qy 181 GTATTATTATTAACCTGGTATTCACACTGTGTGAATCCAGCTTTTAAATAGTGTAAGTA 240
Db |||||

Qy 181 GTATTATTATTAACCTGGTATTCACACTGTGTGAATCCAGCTTTTAAATAGTGTAAGTA 240
Db |||||

Qy 241 AGAAGTCTCTTATATATCTGGGCGAGTATCAACCATTTCCAGCACTGGCTTGCTACT 300
Db |||||

Qy 241 AGAAGTCTCTTATATATCTGGGCGAGTATCAACCATTTCCAGCACTGGCTTGCTACT 300
Db |||||

Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCCAATTTTATTTTCTTAC 360
Db |||||

Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCCAATTTTATTTTCTTAC 360
Db |||||

Qy 361 TTTAAAGAGGAGGTTAAGAGTGTCAATTCGATGTGTGTTGGGGCCCTTTGCTATTTTGG 420
Db |||||

Qy 361 TTTAAAGAGGAGGTTAAGAGTGTCAATTCGATGTGTGTTGGGGCCCTTTGCTATTTTGG 420
Db |||||

Qy 421 GCTTGTCTATCTTTTGTGATAAATGAGATTTGGGGGCAAAAGAAATTTGAAGGA 480
Db |||||

Qy 421 GCTTGTCTATCTTTTGTGATAAATGAGATTTGGGGGCAAAAGAAATTTGAAGGA 480
Db |||||

Qy 481 AACATGACTTTGGAAGTCAAAATTTGAAGAGTCAATTTTCAAAATATGACTGTAAACC 540
Db |||||

Qy 481 AACATGACTTTGGAAGTCAAAATTTGAAGAGTCAATTTTCAAAATATGACTGTAAACC 540
Db |||||

Qy 541 ATGTTAGCAAACTTTAGTACCCCTTCACTCTGACCCCTTCACTCTGACCCCTTCACTCT 600
Db |||||

Qy 541 ATGTTAGCAAACTTTAGTACCCCTTCACTCTGACCCCTTCACTCTGACCCCTTCACTCT 600
Db |||||

; SEQ ID NO 1491
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1330)
; NAME/KEY: CDS
; LOCATION: (201)..(1130)
US-10-292-798-1491

Query Match 100.0%; Score 930; DB 6; Length 1330;

Best Local Similarity 100.0%; Pred. No. 2.2e-245;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGATACTTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db 201 ATGATACTTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 260
QY 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAG 120
Db 261 AATTTTGCTAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAG 320
QY 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 321 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 380
QY 181 GTATTATTATAACTGGTATTCAACTGTGTGTAATCCAGCTTTTAATAGTGTGAAGTA 240
Db 381 GTATTATTATAACTGGTATTCAACTGTGTGTAATCCAGCTTTTAATAGTGTGAAGTA 440
QY 241 AGAACTACTGCTTATAATATCTGGCGAGTGATCAACATTTTCAGCACTGCTTGTCTACT 300
Db 441 AGAACTACTGCTTATAATATCTGGCGAGTGATCAACATTTTCAGCACTGCTTGTCTACT 500
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTATTTTCTTCAAC 360
Db 501 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTATTTTCTTCAAC 560
QY 361 TTAAGAGGAGAGTAAGAGTGTCACTCTGGTGTATGTTGGGGCCCTTGTCTATTGTTG 420
Db 561 TTAAGAGGAGAGTAAGAGTGTCACTCTGGTGTATGTTGGGGCCCTTGTCTATTGTTG 620
QY 421 GCTTGTCACTTTTGTGATAAAATGAATGAGATTGTCGCGACAAAAGAAATTTGAAGGA 480
Db 621 GCTTGTCACTTTTGTGATAAAATGAATGAGATTGTCGCGACAAAAGAAATTTGAAGGA 680
QY 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGCAATGTAATTTTCAAAATATGACTGTAACC 540
Db 681 AACATGACTTTGGAAGATCAAAATGAAGAGTGCAATGTAATTTTCAAAATATGACTGTAACC 740
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
Db 741 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 800
QY 601 TCTTTGTGTAACATCTCAAGAGATGCAGCTCCATGTAAGGATCTCAAGATCCCGAGC 660
Db 801 TCTTTGTGTAACATCTCAAGAGATGCAGCTCCATGTAAGGATCTCAAGATCCCGAGC 860
QY 661 ACCAAGTCCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 861 ACCAAGTCCACATAAAGCTTTGCAAACTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 920
QY 721 TACTTTCTGCTCAATAATGATATGATTTGGAGTTTGGAGTCTGGAAAACAAACCTCTGTC 780
Db 921 TACTTTCTGCTCAATAATGATATGATTTGGAGTTTGGAGTCTGGAAAACAAACCTCTGTC 980
QY 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTTATCCCTTCAATCCACCCATTCATCTGATT 840
Db 981 TTCAATGTTCTGCAAGCTATTAGATTCAGCTTATCCCTTCAATCCACCCATTCATCTGATT 1040
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QY 841 TGGGAAACAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTTTGGCAATGAGGTACTGG 900
Db 1041 TGGGAAACAAGAGCTAAAGCAGACTTTTCTTTTCAGTTTTTGGCAATGAGGTACTGG 1100
QY 901 GTGAAGGAGAGAGAGACTTCATCTCCATAG 930
Db 1101 GTGAAGGAGAGAGAGACTTCATCTCCATAG 1130

RESULT 10

US-09-825-882-11

; Sequence 11, Application US/09825882

; Patent No. US20020094551A1

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME

; FILE REFERENCE: 078003/0279152/EXT

; CURRENT APPLICATION NUMBER: US/09/825,882

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,532

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 60/247,014

; PRIOR FILING DATE: 2000-11-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 930

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-825-882-11

Query Match 91.6%; Score 851.6; DB 3; Length 930;

Best Local Similarity 94.7%; Pred. No. 7.4e-224;

Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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QY 1 ATGATACTTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTGGA 60
Db 1 ATGATACTTTTCTACCCATCATTTTTTCCAGTCTGGTAGTGGTTCTATTTCTATTGGA 60
QY 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAG 120
Db 61 AATTTTGCTAATGGCTTCATAGCACTGGTAAATCCATTGAGTGGTTCAAGAGACAAAG 120
QY 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
Db 121 ATCTCCTTTGCTGACCAAAATTTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGG 180
QY 181 GTATTATTATAACTGGTATTCAACTGTGTGTAATCCAGCTTTTAATAGTGTGAAGTA 240
Db 181 GTATTATTATAACTGGTATTCAACTGTGTGTAATCCAGCTTTTAATAGTGTGAAGTA 240
QY 241 AGAACTACTGCTTATAATATCTGGCGAGTGATCAACATTTTCAGCACTGCTTGTCTACT 300
Db 241 AGAACTACTGCTTATAATATCTGGCGAGTGATCAACATTTTCAGCACTGCTTGTCTACT 300
QY 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTATTTTCTTCAAC 360
Db 301 ACCCTCAGCATATTTTATTTGCTCAAGATTGCCAAATTTCTCCAACTTTATTTTCTTCAAC 360
QY 361 TTAAGAGGAGAGTAAGAGTGTCACTCTGGTGTATGTTGGGGCCCTTGTCTATTGTTG 420
Db 361 TTAAGAGGAGAGTAAGAGTGTCACTCTGGTGTATGTTGGGGCCCTTGTCTATTGTTG 420
QY 421 GCTTGTCACTTTTGTGATAAAATGAATGAGATTGTCGCGACAAAAGAAATTTGAAGGA 480
Db 421 GCTTGTCACTTTTGTGATAAAATGAATGAGATTGTCGCGACAAAAGAAATTTGAAGGA 480
QY 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGCAATGTAATTTTCAAAATATGACTGTAACC 540
Db 481 AACATGACTTTGGAAGATCAAAATGAAGAGTGCAATGTAATTTTCAAAATATGACTGTAACC 540
QY 541 ATGGTAGCAAACTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
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Db 721 TACCTTCTGTCATATGATATCATGTTGGAGTTTGGAGTCTGGAACCAACCTGTC 780
Qy 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCAATCTGATT 840
Db 781 TTCATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCAATCTGATT 840
Qy 841 TGGGGAACAGAGCTAAGCAGACTTTCTTTTCAGTTTCTTTTGGCAATGAGGTACTGG 900
Db 841 TGGGGAACAGAGCTAAGCAGACTTTCTTTTCAGTTTCTTTTGGCAATGAGGTACTGG 900
Qy 901 GTGAAGAGAGAGAGACTTTCATCTCCATAG 930
Db 901 GTGAAGAGAGAGAGACTTTCATCTCCATAG 930

RESULT 14
US-10-724-209-11
; Sequence 11, Application US/10724209
; Publication No. US20040248149A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 100337.54075US
; CURRENT APPLICATION NUMBER: US/10/724,209
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-209-11

Query Match 91.6%; Score 851.6; DB 8; Length 930;
Best Local Similarity 94.7%; Pred. No. 7.4e-224;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 ATGTAACCTTTTCTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTTCTATTGGA 60
Db 1 ATGCAACCTTTTATACCCATCATTTTCCAGTCTGGTAGTGGTTCTATTGTTATTGGA 60
Qy 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTAGTGGTTCAAGAGACAAAAG 120
Db 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTAGTGGTTCAAGAGACAAAAG 120
Qy 121 ATCTCTTTTGTCTGACCAATTCCTACTGCTCTGGCGGTCTCAGAGTTGGTTGCTCTGG 180
Db 121 ATCTCTTTTGTCTGACCAATTCCTACTGCTCTGGCGGTCTCAGAGTTGGTTGCTCTGG 180
Qy 181 GTATTATTATTAACTGGTATTCAACTGTTGTAATCCAGCTTTTAAATAGTCTAGAAGTA 240
Db 181 GTATTATTATTAACTGGTATTCAACTGTTGTAATCCAGCTTTTAAATAGTCTAGAAGTA 240
Qy 241 AGAAGTCTGCTTATAATATCTGGCAGTGATCAACCAATTTCCAGCAACTGGCTTCTACT 300
Db 241 AGAAGTCTGCTTATAATATCTGGCAGTGATCAACCGGCCATTTTCAGCAACTGGCTTCTACT 300
Qy 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCAACTTATTTTCTTTCAC 360
Db 301 ACCCTCAGCATATTTTATTTGCTCAAGATTCGCAATTTCTCAACTTATTTTCTTTCAC 360
Qy 361 TTAAGAGAGAGAGTTAAGAGTCTCAATCTGGTGATGTTGTTGGGCTTTTGTCTTTTGG 420
Db 361 TTAAGAGAGAGAGTTAAGAGTCTCAATCTGGTGATGTTGTTGGGCTTTTGTCTTTTGG 420
Qy 421 GCTTGTCTATCTTTTGTGATAAACAATGAATAGATTTGTGCGGACAAAAGAAATTTGAAGA 480
Db 421 GCTTGTCTATCTTTTGTGATAAACAATGAATAGATTTGTGCGGACAAAAGAAATTTGAAGA 480

Qy 481 AACATGCTTGGAGATCAAAATTTGAAGATGCAATGTACTTTTCAAAATATGACTCTAACC 540
Db 481 AACTTGACTTGGAGATCAAAATTTGAGGATGCAATGTACTTTTCAAAATATGACTCTAACC 540
Qy 541 ATGCTAGCAAACTTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
Db 541 ACCTAGGAACTTTAGTACCCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGT 600
Qy 601 TCTTTGTAAACATCTCAAGAAGATGAGCTCCATGTTAAAGATCTCAAGATCCACAGC 660
Db 601 TCTCTGTAAACATCTCAAGAAGATGAGCTCCATGTTAAAGATCTCAAGATCCACAGC 660
Qy 661 ACCAGGTCACATATAAAGCTTTGCAAACTGTGATCTCTTCTCTCTCTTATGTCGCAAT 720
Db 661 ACCAAGTCCACATAAAGCTTTGCAAACTGTGATCTCTTCTCTCTCTTATGTCGCGGT 720
Qy 721 TACTTTCTGTCCTAATGATATCACTTTGGAGTTTGGAAAGTCTGGAACCAAACTCTGTC 780
Db 721 TACTTTCTGTCCTAATGATATCACTTTGGAGTTTGGAGTCTGGAACCAAACTCTGTC 780
Qy 781 TCTATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCAATCTGATT 840
Db 781 TCTATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCAATCTGATT 840
Qy 841 TGGGGAACAGAGCTAAGCAGACTTTTCTTTCAGTTTCTTGGCAATGAGGTACTGG 900
Db 841 TGGGGAACAGAGCTAAGCAGACTTTTCTTTCAGTTTCTTGGCAATGAGGTACTGG 900
Qy 901 GTGAAGAGAGAGAGACTTTCATCTCCATAG 930
Db 901 GTGAAGAGAGAGAGACTTTCATCTCCATAG 930

RESULT 15
US-10-986-871-11
; Sequence 11, Application US/10986871
; Publication No. US20050069944A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/EXT
; CURRENT APPLICATION NUMBER: US/10/986,871
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/825,882
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-986-871-11

Query Match 91.6%; Score 851.6; DB 9; Length 930;
Best Local Similarity 94.7%; Pred. No. 7.4e-224;
Matches 881; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 ATGTAACCTTTTCTACCCATCATTTTCCAGTCTGGTAGTGGTTACATTTCTATTGGA 60
Db 1 ATGCAACCTTTTATACCCATCATTTTCCAGTCTGGTAGTGGTTCTATTGTTATTGGA 60
Qy 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTAGTGGTTTCAAGAGACAAAAG 120
Db 61 AATTTTGTCTAATGGCTTCATAGCACTGGTAAATTCATTTAGTGGTTTCAAGAGACAAAAG 120
Qy 121 ATCTCTTTTGTCTGACCAATTCCTACTGCTCTGGCGGTCTCAGAGTTGGTTTGTCTGG 180
Db 121 ATCTCTTTTGTCTGACCAATTCCTACTGCTCTGGCGGTCTCAGAGTTGGTTTGTCTGG 180

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Qy 181 GTATTATTATTAAACTGGTATTCAACTGTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Db 181 GTATTATTATTAAATTTGGTATTCAACTGTGTGTGAATCCAGCTTTTAAATAGTGTAGAAGTA 240
Qy 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCACTGGCTTGGCTACT 300
Db 241 AGAACTACTGCTTATAATATCTGGGCACTGATCAACCAATTTTCAGCACTGGCTTGGCTACT 300
Qy 301 ACCCTCAGCAATATTTTATTTCTCAAGATTCGCAATTTCTCAAACTTTTATTTTCTTCAC 360
Db 301 AGCCTCAGCAATATTTTATTTCTCAAGATTCGCAATTTCTCAAACTTTTATTTTCTTCAC 360
Qy 361 TTAAGAGGAGAGTTAAGAGTGTATTTCTGTGTGATGTTGTTGGGCCCTTTGCTATTTTGTG 420
Db 361 TTAAGAGGAGAGTTAAGAGTGTATTTCTGTGTGATGTTGTTGGGCCCTTTTACTATTTTGTG 420
Qy 421 GCTTGTCTATCTTTTGTGATTAACAATGAATGAGATGTGCGGACAAAGAAATTTGAAGGA 480
Db 421 GCTTGTCAACTTTTGTGATTAACAATGAAGAGATGTGACGGAACAAAGAAATATGAAGGA 480
Qy 481 AACATGACTTGGAAAGATCAAAATGAAGAGTGAATGTACTTTTCAAAATATGACTGTAACC 540
Db 481 AACTTGAATTTGGAAGATCAAAATGAGGAGTGCAGTGTACTTTTCAAGATGCGACTGTAACC 540
Qy 541 ATGCTAGCAAACTTTAGTACCCCTTCACTGTGACCCCTTCACTGTGACCCCTTGTATTTTGTAACTCTGT 600
Db 541 ACCTAGCAAACTTTAGTACCCCTTCACTGTGACCCCTTCACTGTGACCCCTTGTATTTTGTAACTCTGT 600
Qy 601 TCTTTGTGTAACATCTCAAGAGATGCGCTCCATGTTAAGGATCTCAAGATCCCAGC 660
Db 601 TCTCTGTGTAACATCTCAAGAGATGCGCTCCATGTTAAGGATCTCAAGATCCCAGC 660
Qy 661 ACCAAGTCCACATAAAAGCTTTGCAAACTGTGATCTCTTCTCTTGTATGTGCCATT 720
Db 661 ACCAAGTCCACATAAAAGCTTTGCAAACTGTGATCTTTTCTCTTGTATGTGCCATT 720
Qy 721 TACTTTCTGTCATAATATGATATCAGTTTGGAGTTTGGAGTCTGGAAACAAACCTGTC 780
Db 721 TACTTTCTGTCATAATATGATATCAGTTTGGAGTTTGGAGTCTGGAAACAAACCTGTC 780
Qy 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCATCCTGATT 840
Db 781 TTCAATGTTCTGCAAGCTATTAGATTCAGCTATCCTTCAATCCACCCATTCATCCTGATT 840
Qy 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTTCTTTTGGCAAAATGAGGTAAGTGG 900
Db 841 TGGGAAACAAAGAGCTAAAGCAGACTTTTCTTTTCTTTTGGCAAAATGAGGTAAGTGG 900
Qy 901 GTGAAGGAGAGAGACTTTCATCTCCATAG 930
Db 901 GTGAAGGAGAGAGCCCTTCATCTCCATAG 930

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Job time : 848 secs

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Db 121 CAAATTTCTCACTGCTCTGGTGTCCAGAGTTGGTTTAACTCTGGGTCATATATTATACA 180
Qy 195 CTGTAATCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254
Db 181 TTGGTATGCAACTGTGTTTAAATTTGGCTTCACATAGATTAGAAATTTTGGTTC 240
Qy 255 TAATATCTGGCAGTGTATCAACCAATTTTCAGCAACTGGCTTGTCTACTACCTTCAGCATATT 314
Db 241 TAATGTCTCAGCAATAACCAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Qy 315 TTATTTGCTCAAGATTCGAATTTCTCAACTTTTAAATTTTCTTCACTTAAAGAGGAGT 374
Db 300 TCATTGCTCAAGACTGCCAATTTCTCAACCTTATTTTCTCCACCTAAAGAAAGGAT 359
Qy 375 TAAGAGTGTCAATCTGGTGTATGTTGTTGGGCTTTTGTCTATTTTGGCTTGTCTATCTTTT 434
Db 360 TAAGAAATGTTGGTTTGGTGTATGCTGTTGGGSCCTTGGTATTTTTCATTGTAATCTTGC 419
Qy 435 TGTGATAAACAATGAATGAGATTTGCGGACAAAAGAAATTTGAAGAAACATGACTTGGAA 494
Db 420 TCTGATAACCAACGCGGTGAGAGTGTGGACAAAAGAAATATGAAGAAATTTGTCTTGGAT 479
Qy 495 GATCAAAATTTGAAGAGTGCATGTACTTTTCAAAATATGACTGTAAACCATGGTAGCAACTT 554
Db 480 GATCAAAATTTGAGGAATGCAATACAGCTTTCAAACTTGACTGTAAACCATGCCAGCAACGT 539
Qy 555 AGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTAAATCTGTTCTTTTGTGTAACA 614
Db 540 CACACCTGACCTGACACTAATATCTTTTCTGCTGTAAATCTATTTCTCATGTAAACA 599
Qy 615 TCTCAAGAAGATGAGCTCCATG 637
Db 600 TGTCAAGAAGATGAGCTCCATG 622

RESULT 4

US-10-301-480-376958
; Sequence 376958, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 376958
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-376958

Query Match 45.0%; Score 418.2; DB 12; Length 622;
Best Local Similarity 81.5%; Pred. No. 4.4e-89;
Matches 508; Conservative 0; Mismatches 113; Indels 2; Gaps 2;

Qy 16 CCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTTGGAATTTTGTCTAATGGC 75
Db 1 CTCATCATTTTATCAATTCCTGGTAGTGTGTCATTGTTCTTGGAAATGTTGCCAATGGC 60
Qy 76 TTCAATAGCATGTTAAATTCATTTAGTGGTTCAAGAGACAAAGATCTCTTTTGTCTGAC 135
Db 61 TTCAATAGCTCTAGTAGTGTCTTTAGTGGGTTAAGACACAAAGATCTCATCAGCTGAC 120
Qy 136 CAAA-TTCTCACTGCTCTGGGCTCTCAGAGTTGGTTTGTCTCTGGGTATATTATAA 194
Db 121 CAAATTTCTCACTGCTCTGGTGTCCAGAGTTGGTTTACTCTGGGTCATATATTATACA 180

Qy 195 CTGTAATCAACTGTGTTGAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254
Db 181 TTGGTATGCAACTGTGTTTAAATTTGGCTTCACATAGATTAGAAATTTTGGTTC 240
Qy 255 TAATATCTGGCAGTGTATCAACCAATTTTCAGCAACTGGCTTGTCTACTACCTTCAGCATATT 314
Db 241 TAATGTCTCAGCAATAACCAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Qy 315 TTATTTGCTCAAGATTCGAATTTCTCAACTTTTAAATTTTCTTCACTTAAAGAGGAGT 374
Db 300 TCATTGCTCAAGACTGCCAATTTCTCAACCTTATTTTCTCCACCTAAAGAAAGGAT 359
Qy 375 TAAGAGTGTCAATCTGGTGTATGTTGTTGGGCTTTTGTCTATTTTGGCTTGTCTATCTTTT 434
Db 360 TAAGAAATGTTGGTTTGGTGTATGCTGTTGGGSCCTTGGTATTTTTCATTGTAATCTTGC 419
Qy 435 TGTGATAAACAATGAATGAGATTTGCGGACAAAAGAAATTTGAAGAAACATGACTTGGAA 494
Db 420 TCTGATAACCAACGCGGTGAGAGTGTGGACAAAAGAAATATGAAGAAATTTGTCTTGGAT 479
Qy 495 GATCAAAATTTGAAGAGTGCATGTACTTTTCAAAATATGACTGTAAACCATGGTAGCAACTT 554
Db 480 GATCAAAATTTGAGGAATGCAATACAGCTTTCAAACTTGACTGTAAACCATGCCAGCAACGT 539
Qy 555 AGTACCTTCACTCTGACCTTACTATCTTTTATGCTGTAAATCTGTTCTTTTGTGTAACA 614
Db 540 CACACCTGACCTGACACTAATATCTTTTCTGCTGTAAATCTATTTCTCATGTAAACA 599
Qy 615 TCTCAAGAAGATGAGCTCCATG 637
Db 600 TGTCAAGAAGATGAGCTCCATG 622

RESULT 5

US-10-301-480-990367
; Sequence 990367, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 990367
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-990367

Query Match 45.0%; Score 418.2; DB 12; Length 622;
Best Local Similarity 81.5%; Pred. No. 4.4e-89;
Matches 508; Conservative 0; Mismatches 113; Indels 2; Gaps 2;

Qy 16 CCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTTGGAATTTTGTCTAATGGC 75
Db 1 CTCATCATTTTATCAATTCCTGGTAGTGTGTCATTGTTCTTGGAAATGTTGCCAATGGC 60
Qy 76 TTCAATAGCATGTTAAATTCATTTAGTGGTTCAAGAGACAAAGATCTCTTTTGTCTGAC 135
Db 61 TTCAATAGCTCTAGTAGTGTCTTTAGTGGGTTAAGACACAAAGATCTCATCAGCTGAC 120
Qy 136 CAAA-TTCTCACTGCTCTGGGCTCTCAGAGTTGGTTTGTCTCTGGGTATATTATAA 194
Db 121 CAAATTTCTCACTGCTCTGGTGTCCAGAGTTGGTTTACTCTGGGTCATATATTATACA 180

```
QY 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACTGCTTA 254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TTGGTATGCAACTGTGTTTAATTTGGCTTCACATAGATTAGAGTTAGAAATTTTGGTTC 240
QY 255 TAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TAATGTCTCAGCAATAACCAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 TTATTTGCTCAAGATGTCGAATTTCTCCAACTTTATTTTCTTCACTTTAAAGAGAGAGT 374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 TCATTTGCTCAAGACTGCGCAATTTCTCCAACTTTATTTTCTCCACCTAAAGAAAGGAT 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 TAAGAGTGTCAATCTGGTGATGTTGTTGGGGCTTTTGCTATTTTGGCTTGTCATCTTTT 434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
360 TAAGAAATGTGTTTGGTGATGCTGTGGGGCCCTTGGTATTTTCAATTTGTAATCTTGC 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 TGTGATAAACATGAATGAGATTTGTCGGACAAAAGAAATTTGAAAGAAACATGACTTGGAA 494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
420 TCTGATAACACCGGTGAGAGTGTGGACAAAAGAAATATGAAGGAAATTTGCTTGGAT 479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 GATCAAAATGAAGATGCAATGTACTTTTCAAAATATGACTGTAAACATGGTAGCAAACTT 554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 GATCAAAATGAGGAATGCAATACAGCTTTCAAACTTTGACTGTAAACATGCCAGCAAACT 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 AGTACCCCTCACTCTGACCTACTATCTTTTATGCTGTTAAATCTCTTTTGTGTAACA 614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
540 CACACCCCTGCACTCTGACACTAATATCTTTCTGCTGTTAATCTATTTCTCCATGTAACA 599
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 TCTCAAGAAGATGCAGCTCCATG 637
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 TGTCAAGAAGATGCAGCTCCATG 622
```

RESULT 6

```
US-10-301-480-376957
; Sequence 376957, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376957
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-376957
```

```
Query Match 44.9%; Score 417.8; DB 12; Length 622;
Best Local Similarity 81.4%; Pred. No. 5.5e-89;
Matches 507; Conservative 1; Mismatches 113; Indels 2; Gaps 2;
```

```
QY 16 CCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTTGGAAATTTTGTCTAATGCG 75
Db 1 CTCATCATTTTATCAATCTGGTAGTGGTTGCAATTTGTTTCTTGGAAATTTTGTCCAAATGCG 60
QY 76 TTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAAGATCTCTTTGCTGAC 135
Db 61 TTCATAGCTCTAGTAGTGTCTTGAAGTGGTTTAAAGACAAAAGATCTCATCAGCTGAC 120
QY 136 CAAA-TTCTCACTGCTCGGGCTCCAGAGTGGTTGCTCTGGGTATTTATTATAA 194
Db 121 CAAATTTCTCACTGCTCGGGTCCAGARTTGGTTTACTCTGGGTCAATATTACA 180
QY 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACTGCTTA 254
```

```
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TTGGTATGCAACTGTGTTTAATTTGGCTTCACATAGATTAGAGTTAGAAATTTTGGTTC 240
QY 255 TAATATCTGGGCACTGATCAACCAATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TAATGTCTCAGCAATAACCAAGCATTTTCAGCATCTGG-GTGTACTAGCCTCAGCATATT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 TTATTTGCTCAAGATGTCGAATTTCTCCAACTTTATTTTCTTCACTTTAAAGAGAGAGT 374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 TCATTTGCTCAAGACTGCGCAATTTCTCCAACTTTATTTTCTCCACCTAAAGAAAGGAT 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 TAAGAGTGTCAATCTGGTGATGTTGTTGGGGCTTTTGCTATTTTGGCTTGTCATCTTTT 434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
360 TAAGAAATGTGTTTGGTGATGCTGTGGGGCCCTTGGTATTTTCAATTTGTAATCTTGC 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 TGTGATAAACATGAATGAGATTTGTCGGACAAAAGAAATTTGAAAGAAACATGACTTGGAA 494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
420 TCTGATAACACCGGTGAGAGTGTGGACAAAAGAAATATGAAGGAAATTTGCTTGGAT 479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 GATCAAAATGAAGATGCAATGTACTTTTCAAAATATGACTGTAAACATGGTAGCAAACTT 554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 GATCAAAATGAGGAATGCAATACAGCTTTCAAACTTTGACTGTAAACATGCCAGCAAACT 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 AGTACCCCTCACTCTGACCTACTATCTTTTATGCTGTTAAATCTCTTTTGTGTAACA 614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
540 CACACCCCTGCACTCTGACACTAATATCTTTCTGCTGTTAATCTATTTCTCCATGTAACA 599
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 TCTCAAGAAGATGCAGCTCCATG 637
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 TGTCAAGAAGATGCAGCTCCATG 622
```

RESULT 7

```
US-10-301-480-990366
; Sequence 990366, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 990366
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-990366
```

```
Query Match 44.9%; Score 417.8; DB 12; Length 622;
Best Local Similarity 81.4%; Pred. No. 5.5e-89;
Matches 507; Conservative 1; Mismatches 113; Indels 2; Gaps 2;
```

```
QY 16 CCCATCATTTTTTCCAGTCTGGTAGTGGTTACATTTGTTATTTGGAAATTTTGTCTAATGCG 75
Db 1 CTCATCATTTTATCAATCTGGTAGTGGTTGCAATTTGTTTCTTGGAAATTTTGTCCAAATGCG 60
QY 76 TTCATAGCACTGGTAAATTCATTTGAGTGGTTCAAGAGACAAAAGATCTCTTTGCTGAC 135
Db 61 TTCATAGCTCTAGTAGTGTCTTGAAGTGGTTTAAAGACAAAAGATCTCATCAGCTGAC 120
QY 136 CAAA-TTCTCACTGCTCGGGCTCCAGAGTGGTTGCTCTGGGTATTTATTATAA 194
Db 121 CAAATTTCTCACTGCTCGGGTCCAGARTTGGTTTACTCTGGGTCAATATTACA 180
QY 195 CTGGTATTCAACTGTGTTGAATCCAGCTTTTAATAGTGTAGAAGTAAGAACTACTGCTTA 254
```

Db 181 TTGGTATGCAACTGTGTTTAAATTTGGCTTCACATAGATTAGAAGTAAGAAATTTTGGTTC 240
Qy 255 TAATACTCGGAGTGATCAACCAATTCAGCAACTGGCTTACTACCTCAGCATATT 314
Db 241 TAATGTCTCAGCAATACCAAGCAATTCAGCATCTGG-GTGTACTAGCCCTCAGCATATT 299
Qy 315 TTATTTGCTCAAGATTGCCAAATTCCTCAACTTTATTTTCTTCACCTAAAGAGGAGT 374
Db 300 TCAATTTGCTCAGACTGCCAAATTCCTCAACTTTATTTTCTCCACCTAAAGAAAGGAT 359
Qy 375 TAAGAGTGTCAATTCGTGTGATGTTGGGGCCCTTTGCTATTTTGGCTTGTCACTTTT 434
Db 360 TAAGAATGTTGGTTTGGTGTGATGCTTTGGGGCCCTTTGCTATTTTTCATTTGTAATCTTGC 419
Qy 435 TGTGATAAACAATGAGATGTTGGCGGACAAAGAAATTTGAAGGAAACATGACTTGGAA 494
Db 420 TCTGATAACCAACCGGTGAGAGTGTGGACAAAAGAAATATCAAGGAAATTTGTCTTGGAT 479
Qy 495 GATCAAAATTCAGAGTGCATGACTTTTCAAAATATGACTGTAAACCATGTTAGCAAACTT 554
Db 480 GATCAAAATTCAGGAATGCATACAGCTTTCAAACTTGACTGTAAACCATGCGCAAACTG 539
Qy 555 AGTACCCCTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGTTTGTGTAACA 614
Db 540 CACACCCCTGCACTCTGACACTAATACTTTTCTGCTGTTTATCTATTTCTCCATGTAACA 599
Qy 615 TCTCAAGAAGATGAGCTCCATG 637
Db 600 TGTCAAGAAGATGAGCTCCATG 622

RESULT 8

US-09-925-065A-300419
; Sequence 300419, Application US/09925065A
; Publication No. US20040181048A1

GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300419

LENGTH: 619

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-300419

Query Match 44.8%; Score 416.4; DB 7; Length 619;
Best Local Similarity 81.5%; Pred. No. 1.2e-88;
Matches 505; Conservative 1; Mismatches 112; Indels 2; Gaps 2;

Qy 16 CCCATCAATTTTCCAGTCTGGTAGTGTTCATCAATTTGTTATGGAATTTTGTCTAATGGC 75
Db 1 CTCATCAATTTATCAATTTCTGGTAGTGTTCATCAATTTGTTATGGAATTTTGTCTAATGGC 60
Qy 76 TTCATAGACTGGTAAATTCATTTGAGTGTTCAGAGACAAAGATCTCTTGTCTGAC 135
Db 61 TTCATAGCTCTAGTAGGTGTCCTTGGTGGGTGAAGACACAAAAGATCTCATCAGCTGAC 120
Qy 136 CAAA-TTCTCACTGCTCTGGCGGTCTCAGAGTTGGTTTGTCTCTGGGTATTATTATTA 194

Db 121 CAAATTTCTACAGTCTGGTGGTGTCCAGAGTTGGTTTACTCTGGGTCAATATTATTA 180
Qy 195 CTGGTATTCAACTGTGTGTAATCCAGCTTTTAAATAGTGTAGAAGTAAGAACTACTGCTTA 254
Db 181 TTGGTATGCAACTGTGTGTTAAATTTGGCTTCACATAGATTAGAAGTAAGAAATTTTGGTTC 240
Qy 255 TAATATCTGGGCAAGTGTATCAACCAATTTTCAGCAACTGGCTTACTACCTCAGCATATT 314
Db 241 TAATGTCTCAGCAATACCAAGCAATTCAGCAATCTGG-GTGTACTAGCCCTCAGCATATT 299
Qy 315 TTATTTGCTCAAGATTGCCAAATTTCTCAACTTTATTTTCTTCACCTAAAGAGGAGT 374
Db 300 TCAATTTGCTCAGACTGCCAAATTTCTCAACTTTATTTTCTCCACCTAAAGAAAGGAT 359
Qy 375 TAAGAGTGTCAATTCGTGTGATGTTGGGGCCCTTTGCTATTTTGGCTTGTCACTTTT 434
Db 360 TAAGAATGTTGGTTTGGTGTGATGCTTTGGGGCCCTTTGCTATTTTTCATTTGTAATCTTGC 419
Qy 435 TGTGATAAACAATGAGATGTTGGCGGACAAAGAAATTTGAAGGAAACATGACTTGGAA 494
Db 420 TCTGATAAACCACCGGTGAGAGTGTGGGACAAAAGAAATATGAAGGAAATTTGTCTTGGAT 479
Qy 495 GATCAAAATTCAGAGTGCATGACTTTTCAAAATATGACTGTAAACCATGTTAGCAAACTT 554
Db 480 GATCAAAATTCAGGAATGCATACAGCTTTCAAACTTGACTGTAAACCATGCGCAAACTG 539
Qy 555 AGTACCCCTCACTCTGACCTACTATCTTTTATGCTGTTAATCTGTTTGTGTAACA 614
Db 540 CACACCCCTGCACTCTGACACTAATACTTTTCTGCTGTTTATCTATTTCTCCATGTAACA 599
Qy 615 TCTCAAGAAGATGAGCTCC 634
Db 600 TGTCAAGAAGATGAGCTCC 619

RESULT 9

US-09-925-065A-300418
; Sequence 300418, Application US/09925065A
; Publication No. US20040181048A1

GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300418

LENGTH: 619

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-300418

Query Match 44.6%; Score 415.2; DB 7; Length 619;
Best Local Similarity 81.5%; Pred. No. 2.3e-88;
Matches 505; Conservative 0; Mismatches 113; Indels 2; Gaps 2;

Qy 16 CCCATCAATTTTCCAGTCTGGTAGTGTTCATCAATTTGTTATGGAATTTTGTCTAATGGC 75
Db 1 CTCATCAATTTATCAATTTCTGGTAGTGTTCATCAATTTGTTATGGAATTTTGTCTAATGGC 60

[illegible]

```

RESULT 10
US-09-925-065A-300417
; Sequence 300417, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 300417
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-300417

```

| | | | |
|----|-----|---|-----|
| Qy | 16 | CCCATCAATTTTTCAGAGCTCGGTAGTGGTTACATTTGTTATTGGAAATTTTGCTAATGCG | 75 |
| Db | 1 | CTCATCAATTTTATCAATCTCGTAGTGTTCATTTGTTCTGGAAATGTTTGCCAATGCG | 60 |
| Qy | 76 | TTCATAGCAGCTGGTAAATTCATTTAGTGGTTCAAGAGACAAAAGATCTCCTTTGCTGAC | 135 |
| Db | 61 | TTCATAGCTCTAGTAGGTGTCCTTGAGTGGGTTAAGACACAAAGATCTCATCAGCTGAC | 120 |
| Qy | 136 | CAAA--TTCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTTGCTCTGGGTATTATTAATAA | 194 |
| Db | 121 | CAAAATTTCTACTGCTCTGGTGGTGTCCAGARTTGGTTTACTCTGGGTCAATATTATACA | 180 |
| Qy | 195 | CTGGTATTCAACTGTGTGTAATCAGCTTTTAAATAGTGTAGAGTAAGAACTACTGCTTA | 254 |
| Db | 181 | TTGGTATGCAACTGTGTTTAAATTTGGCTTTCATAGATTGAAGTAAAGATTTTGGTTTC | 240 |
| Qy | 255 | TAAATCTGGGCACTGATCAACCAATTTCAAGCAATGGGCTTGCTACTACCTCAGCATATT | 314 |
| Db | 241 | TAAATGCTCAGCAATAACCAAGCATTTTCAGCATCTGG--GTGTTACTAGCCTCAGCATATT | 299 |
| Qy | 315 | TTATTTGCTCAAGATGCGCAATTTCTCAAATTTATTTTTCTTCACTTAAGAGAGAGT | 374 |
| Db | 300 | TCAATTTGCTCAAGACTGCGCAATTTCTCCAACCTTATTTTCTCCAACCTTAAGAAAGAT | 359 |
| Qy | 375 | TAAAGTGTCAATCTCTGTGTGATGTTGTGGGGCCCTTGCTATTTTGGCTTGTCATCTTTT | 434 |
| Db | 360 | TAGAAATTTGGTTGGTGTGCTGTTGGGGCCCTTGGTATTTTTTCATTTGTAAATCTTGC | 419 |
| Qy | 435 | TGTGATAAACATGAATGAGATTGTGCGGACAAAAGATTTGAAGGAAACATGACTTGGAA | 494 |
| Db | 420 | TCTGATAACCAACGGGTGAGAGTGTGTGACAAAAGATATGAAGGAAATTTGCTCTGGAT | 479 |
| Qy | 495 | GATCAAAATTTGAAGAGTGCATGTTCTTTTCAAATATGACTGTAAACCATGGTAGCAACTT | 554 |
| Db | 480 | GATCAAAATTTAGGAATGCAATACAGCTTTTCAAACTTGACTGTAAACCATGCCAGCAACGT | 539 |
| Qy | 555 | AGTACCCTTCACTCTGACCCCTACTATCTTTTATGCTGTTAATCTGTTCTTTGTGTAAACA | 614 |
| Db | 540 | CACACCCCTGCACTCTGACACTTAATATCTTTTCTGCTGTTAATCTATTTCTCCATGTAAACA | 599 |
| Qy | 615 | TCTCAAGAAGATGAGCTCC | 634 |
| Db | 600 | TGTCAAGAAGATGAGCTCC | 619 |

```

RESULT 11
US-10-301-480-250660/c
; Sequence 250660, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250660
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-250660

```

Query Match 44.2%; Score 411; DB 12; Length 525;
Best Local Similarity 86.3%; Pred. No. 2.2e-87;
Matches 453; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

| | | | |
|-----|----|---|-----|
| 136 | Qy | CAAAATCTCACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATATTATTAAAC | 195 |
| 525 | Db | CAAAATCTCACTGCTCTGGCGGTCTCCAGAAATGGTTTGGCTCTGGGCATTAATATTAAAT | 466 |
| 196 | Qy | TGGTATTCAACTGTGTGAAATCCAGCTTTTAACTGCTAGAACTAAGAACTACTGCTTAT | 255 |
| 465 | Db | TGGTATTAACTGTGTGAAATCCAGCTTTTATAGTGTAGAAATTAAGAAATTACTTCTTAT | 406 |
| 256 | Qy | AATATCTGGGCAGTGAATCAACCATTTTCAGCAACTGGCTTGGCTACTACCTCAGCATATTTT | 315 |
| 405 | Db | AATGGCTGGGTGTAAACCAATTTTCAGCATGTGGCTTGTGCTAAACCTCAGCATATTTT | 346 |
| 316 | Qy | TATTTGCTCAAGATGCGAAATTTCTCCAATTTATTTTTTCTCACTTAAAGAGGAGAGTT | 375 |
| 345 | Db | TATTTGCTCAAGATGCGAAATTTCTCCAACCTCTCTTTTCTTCAATTAAGAGGAGAGTT | 286 |
| 376 | Qy | AAGAGTGTCAATCTGGTGATGTGTGTGGGGCCCTTTGCTATTTTTTGGCTTGTGCATCTTTT | 435 |
| 285 | Db | AGGAGTGTCAATCTGGTGATACTGTGTGGGAGCTTTTGATATTTTTTGGTTTGTGCATCTTCTT | 226 |
| 436 | Qy | GTGATAAACATGAATGAGATTGTGGCGGCAAAAGAAATTTGAAGGAAACATGACTTGGAG | 495 |
| 225 | Db | GTGGCAAAACATGGATGAGATGTGGCGAAGAAATATGAAGGAAACATGACTGGGAG | 166 |
| 496 | Qy | ATCAAAATTGAAGAGTGCAATGTACTTTTCAAATATGACTGTAAACCATGGTAGCAACATTA | 555 |
| 165 | Db | ATGAAATTGAGGAATACAGTACATCTTTTCATATTTTGACTGTAACTACCCATATGGAGCTTC | 106 |
| 556 | Qy | GTACCCCTTCACTCTGACCCCTACTATCTTTTATATGCTGTGTTAACTGTTCTTTGTGTAAACAT | 615 |
| 105 | Db | ATACCCCTTACTCTGTCCCTGATATCTTTTCTGTATGCTAACTGTTCTCTGTRTAAACAT | 46 |
| 616 | Qy | CTCAAGAAGATGCAAGTCCATGGTAAAGGATCTCAAGATCCCAGC | 660 |
| 45 | Db | CTCAAGAAGATGCAAGTCCATGGGAAGGATCGCAAGATCTCAGC | 1 |

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RESULT 12
US-10-301-480-864069/c
; Sequence 864069, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 864069
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-864069

```

| | | | |
|---|-----|--|-----|
| Db | 405 | AATGCCTGGGTTGTAAACCAACATTTTCAGCATGTGGCTTGCTGTAAACCTCAGCATATTT | 346 |
| Qy | 316 | TATTTGCTCAAGATTGCGCAATTTCTCCAACTTTATTTTCTTCTCACTTAAAGAGGAGAGTT | 375 |
| Db | 345 | TATTTGCTCAAGATTGCGCAATTTCTCCAACTTTCTTCTTCTCATTTAAAGAGGAGAGTT | 286 |
| Qy | 376 | AAGAGTGTCAATCTTGGTGATGTTGTGGGGCCTTTGGCTATTTTGGCTTGTGCATCTTTTT | 435 |
| Db | 285 | AGGAGTGTCAATCTTGGTGATGTTGTGGGGCCTTTGTATATTTTGGTTTGTTCATCTTCTT | 226 |
| Qy | 436 | GTGATTAACATGAATGAGATTGTGGGACAAAGAAATTTGAAGGAACATGACTTTGGAG | 495 |
| Db | 225 | GTGGCAACATGGATGAGAGTATGTGGGCAGAGAATATGAAGGAACATGACTGGGAG | 166 |
| Qy | 496 | ATCAAAATTGAAGAGTGCAAATGACTTTTCAAATATGACTGTAACCATGGTAGCAACATTA | 555 |
| Db | 165 | ATGAAATTGAGGAATACAGTACATCTTTTCATATTTGACTGTAACTACCTATGGAGCTTC | 106 |
| Qy | 556 | GTACCTTCACTCTGACCTACTATCTTTTATGCTGTGTTAACTGTCTTGTGTAAACAT | 615 |
| Db | 105 | ATACCTTTTACTCTGTCCCTGATATCTTTCTGATGCTAACTCTGTCTCTGTGTAAACAT | 46 |
| Qy | 616 | CTCAAGAGATGCGAGCTCCATGGTAAAGGATCTCAAGATCCGAGC | 660 |
| Db | 45 | CTCAAGAGATGCGAGCTCCATGGAGAGGATCGCAAGATCTCAGC | 1 |
| RESULT 13 | | | |
| US-10-301-480-251369/c | | | |
| ; Sequence 251369, Application US/10301480 | | | |
| ; Publication No. US20060057564A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Wang, David G. | | | |
| ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorph | | | |
| ; TITLE OF INVENTION: in the Human Genome | | | |
| ; FILE REFERENCE: 108827.137 | | | |
| ; CURRENT APPLICATION NUMBER: US/10/301,480 | | | |
| ; CURRENT FILING DATE: 2002-11-21 | | | |
| ; PRIOR APPLICATION NUMBER: US 10/215,598 | | | |
| ; PRIOR FILING DATE: 2002-08-09 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/311,695 | | | |
| ; PRIOR FILING DATE: 2001-08-10 | | | |
| ; NUMBER OF SEQ ID NOS: 1226818 | | | |
| ; SOFTWARE: FastSeq for Windows Version 4.0 | | | |
| ; SEQ ID NO 251369 | | | |
| ; LENGTH: 612 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapien | | | |
| US-10-301-480-251369 | | | |

| Query Match | 42.9%; | Score 398.6; | DB 12; | Length 612; |
|-----------------------|-----------------|---|-----------|-------------|
| Best Local Similarity | 81.3%; | Pred. No. 1.9e-84; | | |
| Matches 497; | Conservative 1; | Mismatches 110; | Indels 3; | Gaps 3; |
| Qy | 135 | CCAAATTCACAGTCTCGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTATTATTAAA | 194 | |
| Db | 610 | CAAAATTCACAGTCTCGTGGTGTCCAGAAATGGTTTAACTCTGGGTCAATATTATTACA | 551 | |
| Qy | 195 | CTGGTATTCAACTGTGTGTAATCCAGCTTTTAAATAGTGAAGTAAAGAACTACTGCTTA | 254 | |
| Db | 550 | TTGGTATCAACTGTGTTTAAATTTGGCTTCATATAGATTAGAAGTAAAGAAATTTTGGTTC | 491 | |
| Qy | 255 | TAATATCTGGGCAGTGATCAACCATTTTCAGCAACTGGCTTGCTACTACCTCAGCATATT | 314 | |
| Db | 490 | TAATGTCTCAGCAATAACCAAGCATTTTCAGCATSTGG-GTGTTACTAGCCTCAGCATATT | 432 | |
| Qy | 315 | TTATTTGCTCAAGATTGCCAATTTCTCCAACCTTTATTTTCTTCACTTAAAGAGGAGAT | 374 | |
| Db | 431 | TCAATTTGCTCAAGCTGCCAATTTCTCCAACCTTTATTTTCTCCAACCTAAAGAGGAGAT | 372 | |
| Qy | 375 | TAAGAGTGTCAATTCCTGGTGAATGTTGTGGGGCCCTTTGCTATTATTTTGGCTTGTCACTCTTT | 434 | |

Db 371 TAAAGATGTTGGTTGGTGATGCTGTTGGGGCCCTGGGTATTTTTCATTTGTAATCTTGC 312
QY 435 TGTGATAACATGAATGAGATTGTGGGACAAAGAAATTTGAAGGAACATGACTTGGAA 494
Db 311 TCTGATAACACCGGTGAGAGTGTGGGACAAAGAAATATGAAGAAATTTGCTTGGAT 252
QY 495 GATCAAAATTGAAGAGTGAATGCTATTTTCAAAATATGACTGTAAACCATGTTAGCAAACTT 554
Db 251 GATCAAAATTGAGGATGCATACAGCTTTCAAACTTTGACTGTAAACCATGCCAGCAACGT 192
QY 555 AGTACCCCTTCACTCTGACCCCTACTATCTTTTATATGCTGTTTAAATCTGTTCTTTGTGTAACA 614
Db 191 CACACCCCTGCACTCTGACACTAATATCTTTTCTGCTGTTAAATCTATTTCTCCATGTAAACA 132
QY 615 TCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCAGCAACAAGGT-CCACA 673
Db 131 TGTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCTCAGCAACAAGGTGCAACA 72
QY 674 TAAAGCTTTGCAAACTGTGATCT-CTTCCCTCTTGTATGTCCTATTTACTTTCTGTCC 732
Db 71 TAAAGCTTTGCAAACTGGGATCTCCCTTCGTAATGTTATTTGCCATTTACTTTCTGTGT 12
QY 733 ATAATGATATC 743
Db 11 ATAATCACATC 1

RESULT 14
US-10-301-480-864778/c
; Sequence 864778, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 864778
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-864778

Query Match 42.9%; Score 398.6; DB 12; Length 612;
Best Local Similarity 81.3%; Pred. No. 1.9e-84;
Matches 497; Conservative 1; Mismatches 110; Indels 3; Gaps 3;
QY 135 CCAAAATTCCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTTATTATAA 194
Db 610 CAAATTTCTACTGCTCTGGGTGTCAGAAATGGTTTACTCTGGTCATATTAATACA 551
QY 195 CTGGTATTCACCTGTGTTGAATCCAGCTTTTAAATAGTGTAGAGTAAGAACTACTGCTTA 254
Db 550 TTGGTATGCACTGTGTTTAAATTTGGCTTCATATAGATTAGAAGTAAGAAATTTTGGTTC 491
QY 255 TAAATCTGGGAGTGATCAACCATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314
Db 490 TAAATGCTCAGCAATTAACCAAGCATTTTCAGCATGTGG-GTGTACTAGCCTCAGCATATT 432
QY 315 TTATTTGCTCAAGATGCGCAATTTCTCCAACTTTATTTTCTTCACTTTAAAGAGGAGAT 374
Db 431 TCATTTGCTCAAGACTGCGCAATTTCTCCAACTTTATTTTCTCCACCTAAAGAGGAT 372
QY 375 TAAAGATGTCATCTGTTGATGTTGTTGGGCTTTGCTATTTTGGCTTTGTCATCTTTT 434
Db 371 TAAAGATGTTGGTTGGTGATGCTGTTGGGGCCCTGGGTATTTTTCATTTGTAATCTTGC 312

QY 435 TGTGATAACATGAATGAGATTGTGGGACAAAGAAATTTGAAGGAACATGACTTGGAA 494
Db 311 TCTGATAACACCGGTGAGAGTGTGGGACAAAGAAATATGAAGAAATTTGCTTGGAT 252
QY 495 GATCAAAATTGAAGAGTGAATGCTATTTTCAAAATATGACTGTAAACCATGTTAGCAAACTT 554
Db 251 GATCAAAATTGAGGATGCATACAGCTTTCAAACTTTGACTGTAAACCATGCCAGCAACGT 192
QY 555 AGTACCCCTTCACTCTGACCCCTACTATCTTTTATATGCTGTTTAAATCTGTTCTTTGTGTAACA 614
Db 191 CACACCCCTGCACTCTGACACTAATATCTTTTCTGCTGTTAAATCTATTTCTCCATGTAAACA 132
QY 615 TCTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCCAGCAACAAGGT-CCACA 673
Db 131 TGTCAAGAAGATGCAGCTCCATGTTAAAGGATCTCAAGATCTCAGCAACAAGGTGCAACA 72
QY 674 TAAAGCTTTGCAAACTGTGATCT-CTTCCCTCTTGTATGTCCTATTTACTTTCTGTCC 732
Db 71 TAAAGCTTTGCAAACTGGGATCTCCCTTCGTAATGTTATTTGCCATTTACTTTCTGTGT 12
QY 733 ATAATGATATC 743
Db 11 ATAATCACATC 1

RESULT 15
US-10-301-480-251370/c
; Sequence 251370, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251370
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-251370

Query Match 42.7%; Score 397.4; DB 12; Length 612;
Best Local Similarity 81.3%; Pred. No. 3.7e-84;
Matches 497; Conservative 0; Mismatches 111; Indels 3; Gaps 3;
QY 135 CCAAAATTCCTACTGCTCTGGCGGTCTCCAGAGTTGGTTGCTCTGGGTATTTATTATAA 194
Db 610 CAAATTTCTACTGCTCTGGGTGTCAGAAATGGTTTACTCTGGTCATATTAATACA 551
QY 195 CTGGTATTCACCTGTGTTGAATCCAGCTTTTAAATAGTGTAGAGTAAGAACTACTGCTTA 254
Db 550 TTGGTATGCACTGTGTTTAAATTTGGCTTCATATAGATTAGAAGTAAGAAATTTTGGTTC 491
QY 255 TAAATCTGGGAGTGATCAACCATTTTCAGCAACTGGCTTGCTACTACCCCTCAGCATATT 314
Db 490 TAAATGCTCAGCAATTAACCAAGCATTTTCAGCATGTGG-GTGTACTAGCCTCAGCATATT 432
QY 315 TTATTTGCTCAAGATGCGCAATTTCTCCAACTTTATTTTCTTCACTTTAAAGAGGAGAT 374
Db 431 TCATTTGCTCAAGACTGCGCAATTTCTCCAACTTTATTTTCTCCACCTAAAGAGGAT 372
QY 375 TAAAGATGTCATCTGTTGATGTTGTTGGGCTTTGCTATTTTGGCTTTGTCATCTTTT 434
Db 371 TAAAGATGTTGGTTGGTGATGCTGTTGGGGCCCTGGGTATTTTTCATTTGTAATCTTGC 312

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